

GenCore version 5.1.6									
Title:	OM protein - protein search, using sw model								
Perfect score:	US-10-003-211-1								
Sequence:	1 SQPQAVPPYVSENQTCRDOE.....QSDFICKNPLIEPFPEMST 197								
Scoring table:	BLOSUM62								
Gapop	10.0 , Gapext 0.5								
Searched:	1586107 seqs, 282547505 residues								
Total number of hits satisfying chosen parameters:	1586107								
Minimum DB seq length:	0								
Maximum DB seq length:	2000000000								
Post-processing: Minimum Match 0%									
Maximum Match 100%									
Listing first 45 summaries									
Database :	A_Geneseq_29Jan04:*								
1:	geneseqp1980s:*								
2:	geneseqp2000s:*								
3:	geneseqp2001s:*								
4:	geneseqp2002s:*								
5:	geneseqp2003as:*								
6:	geneseqp2004as:*								
7:	geneseqp2004as:*								
8:	geneseqp2004as:*								
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
result No.	Score	Query	Match Length	DB ID	Description	RESULT 1	ID	AAW23220 standard; protein; 197 AA.	
1	1133	100.0	197	2 AAW23220	AAw23220 Extracell	AAW23220	XX	AAW23220 standard; protein; 197 AA.	
2	1133	100.0	197	2 AAY31326	Aay31326 Human lym	XX	DE	Extracellular domain of human lymphotoxin beta receptor.	
3	1133	100.0	435	6 ABR4020	ABP96137 Human TNF	XX	KW	Human; lymphotoxin beta; receptor; blocking agent; extracellular; ligand binding; domain; treatment; mfi cell; immune response; delayed; hypersensitivity; contact; tuberculin; granulomatous; graft versus host; disease; organ rejection; autoimmune; disorder; multiple sclerosis; insulin dependent diabetes; uveitis; cytokine; sympathetic ophthalmia; porosisis; listeria; Toxoplasma; infection; Mycobacterium; abnormal; lymphoid organ; development.	
4	1133	100.0	435	6 ABR89821	ABP96136 Human TNF	XX	KW		
5	1133	100.0	435	6 ABR98136	ABP96136 Human TNF	XX	KW		
6	1129	99.5	399	7 ADG42855	ADG42856 REBMAP pro	XX	KW		
7	1108	97.8	416	7 ADG42855	ADG49700 Extracell	XX	KW		
8	987	87.1	170	6 ADG49700	ADG49700 Human tum	XX	KW		
9	971	68.0	415	6 ABP96139	ABP96139 Human tum	XX	KW		
10	771	68.0	415	6 ABP96138	ABP96138 Mouse lym	XX	KW		
11	456	40.2	77	2 AAW94642	AAW94642 TNFR ext	XX	KW		
12	456	40.2	77	4 AAB69194	AAB69194 Human tum	XX	KW		
13	381.5	33.7	305	5 ABB41995	ABB41995 Human ova	XX	KW		
14	311.5	27.8	518	2 ABB51003	ABB51003 Sequence	XX	KW		
15	311.5	27.8	659	4 ABB37103	ABB37103 Concataine	XX	KW		
16	309	27.3	461	2 ABB72504	ABB72504 Concataine	XX	KW		
17	307	27.1	720	6 ABB37101	ABB37101 Concataine	XX	KW		
18	305	22.5	3 AAY77463	AAY77463 Primate p	XX	KW			
19	305	22.5	6 AAO26525	AO26526 Human tum	XX	KW			
20	305	22.5	6 AAO26525	AO26526 Human tum	XX	KW			
21	26.9	22.7	422	4 AAB36981	AAB36981 Tfrf2 pro	XX	KW		
22	26.9	22.7	422	2 AAW52270	AAW52270 Human sol	XX	KW		
23	26.9	22.5	2 AAW89234	AAW89234 Tumour ne	XX	KW			
24	305	23.5	3 AAY54440	AAY54440 Anilic aci	XX	KW			
25	26.9	23.5	3 AAY54443	AAY54443 Wild type	XX	KW			
ALIGNMENTS									
1	AAW23220	AAW23220 standard; protein; 197 AA.	AAW23220	AAW23220 standard; protein; 197 AA.	AAW23220	AAW23220	XX	AAW23220 standard; protein; 197 AA.	
2	XX	29-OCT-1997 (first entry)	XX	XX	XX	XX	XX		
3	XX	19-JUL-1996; 96WO-US012010.	XX	PR	PR	PR	XX	19-JUL-1996; 96WO-US012010.	
4	XX	21-JUL-1995; 95US-00505606.	XX	PA	PA	PA	XX	21-JUL-1995; 95US-00505606.	
5	XX	(BIOJ ) BIOGEN INC.	XX	PT	PT	PT	XX	(BIOJ ) BIOGEN INC.	
6	XX	Browning JL, Benjamin CD, Hochman PS;	XX	DR	DR	DR	XX	Browning JL, Benjamin CD, Hochman PS;	
7	XX	WPI; 1997-13237/12.	XX	XX	XX	XX	XX	WPI; 1997-13237/12.	
8	XX	Compositions comprising lymphotoxin-beta receptor blocking agent - used to treat auto:immune diseases, e.g. sclerosis, insulin-dependent diabetes, etc.	XX	PT	PT	PT	XX	Compositions comprising lymphotoxin-beta receptor blocking agent - used to treat auto:immune diseases, e.g. sclerosis, insulin-dependent diabetes, etc.	
9	XX	Example 1; Page 55-56; 76pp; English.	XX	PS	PS	PS	XX	Example 1; Page 55-56; 76pp; English.	
10	XX	The present sequence, a human lymphotoxin beta receptor (LT-beta-R) blocking agent, comprises the extracellular ligand binding domain of the human LT-beta-R up to the transmembrane region. It can be used to treat a hyper sensitivity reaction, preferably contact, tuberculin type or granulomatous hypersensitivity, graft versus host disease, organ rejection or an autoimmune disorder, i.e.: multiple sclerosis, insulin dependent diabetes, sympathetic ophthalmia, uveitis and psoriasis. It can	CC	CC	CC	CC	XX	The present sequence, a human lymphotoxin beta receptor (LT-beta-R) blocking agent, comprises the extracellular ligand binding domain of the human LT-beta-R up to the transmembrane region. It can be used to treat a hyper sensitivity reaction, preferably contact, tuberculin type or granulomatous hypersensitivity, graft versus host disease, organ rejection or an autoimmune disorder, i.e.: multiple sclerosis, insulin dependent diabetes, sympathetic ophthalmia, uveitis and psoriasis. It can	
11	XX	human LT-beta-R	CC	CC	CC	CC	XX	human LT-beta-R	
12	XX	mediated immune response which contributes to a delayed type	CC	CC	CC	CC	XX	mediated immune response which contributes to a delayed type	
13	XX	hypersensitivity reaction, preferably contact, tuberculin type or	CC	CC	CC	CC	XX	hypersensitivity reaction, preferably contact, tuberculin type or	
14	XX	granulomatous hypersensitivity, graft versus host disease, organ	CC	CC	CC	CC	XX	granulomatous hypersensitivity, graft versus host disease, organ	
15	XX	rejection or an autoimmune disorder, i.e.: multiple sclerosis, insulin	CC	CC	CC	CC	XX	rejection or an autoimmune disorder, i.e.: multiple sclerosis, insulin	
16	XX	dependent diabetes, sympathetic ophthalmia, uveitis and psoriasis. It can	CC	CC	CC	CC	XX	dependent diabetes, sympathetic ophthalmia, uveitis and psoriasis. It can	
17	XX	be used to treat a hyper sensitivity reaction, preferably contact, tuberculin type or granulomatous hypersensitivity, graft versus host disease, organ	CC	CC	CC	CC	XX	be used to treat a hyper sensitivity reaction, preferably contact, tuberculin type or granulomatous hypersensitivity, graft versus host disease, organ	
18	XX	rejection or an autoimmune disorder, i.e.: multiple sclerosis, insulin	CC	CC	CC	CC	XX	rejection or an autoimmune disorder, i.e.: multiple sclerosis, insulin	
19	XX	dependent diabetes, sympathetic ophthalmia, uveitis and psoriasis. It can	CC	CC	CC	CC	XX	dependent diabetes, sympathetic ophthalmia, uveitis and psoriasis. It can	
20	XX	be used to treat a hyper sensitivity reaction, preferably contact, tuberculin type or granulomatous hypersensitivity, graft versus host disease, organ	CC	CC	CC	CC	XX	be used to treat a hyper sensitivity reaction, preferably contact, tuberculin type or granulomatous hypersensitivity, graft versus host disease, organ	
21	XX	rejection or an autoimmune disorder, i.e.: multiple sclerosis, insulin	CC	CC	CC	CC	XX	rejection or an autoimmune disorder, i.e.: multiple sclerosis, insulin	
22	XX	dependent diabetes, sympathetic ophthalmia, uveitis and psoriasis. It can	CC	CC	CC	CC	XX	dependent diabetes, sympathetic ophthalmia, uveitis and psoriasis. It can	
23	XX	be used to treat a hyper sensitivity reaction, preferably contact, tuberculin type or granulomatous hypersensitivity, graft versus host disease, organ	CC	CC	CC	CC	XX	be used to treat a hyper sensitivity reaction, preferably contact, tuberculin type or granulomatous hypersensitivity, graft versus host disease, organ	
24	XX	rejection or an autoimmune disorder, i.e.: multiple sclerosis, insulin	CC	CC	CC	CC	XX	rejection or an autoimmune disorder, i.e.: multiple sclerosis, insulin	
25	XX	dependent diabetes, sympathetic ophthalmia, uveitis and psoriasis. It can	CC	CC	CC	CC	XX	dependent diabetes, sympathetic ophthalmia, uveitis and psoriasis. It can	

also be used to treat conditions exacerbated by the activities of Th-1 type cytokines, or Listeria, Toxoplasma or Mycobacterium infection. Its useful to selectively or partially block the LT-beta-R pathway may be useful in the treatment of abnormal lymphoid organ development associated with misexpression or overexpression of signalling by the LT-beta-R pathway. The present LT-beta-R blocking agent is capable of selectively inhibiting Th1, but not Th2 cell dependent immune effector mechanisms. As the cytokines can inhibit Th2 cell dependent responses, the present LT-

CC interaction between lymphotoxin (LT)-beta and its receptor. An inhibitor CC of the interaction between LT-beta and its receptor can be administered CC for altering the survival or maintenance of Follicular dendritic cells in CC a subject and for altering the architecture of the organs of the immune CC system. The method is useful for treating tumours, specifically CC follicular lymphomas. It offers an alternative therapy for those with CC tumours resistant to traditional chemotherapy. The present sequence CC represents the extracellular region of the human LTbeta-receptor and CC comprises the ligand binding domain.

Sequence	197 AA;	SQ
Query Match	100.0%	Score 1133; DB 2; Length 197;
Best Local Similarity	100.0%; Pred. No. 1e-78;	Mismatches 0;
Matches 197; Conservative 0;	Indels 0;	Gaps 0;
QY	1 SQPQAAPPVYASENOTCRDQEKEYFEPHQHICCSQCPGPYVSAKCSRIRDTVCATCAENS	60
Db	1 SQPQAAPPVYASENOTCRDQEKEYFEPHQHICCSQCPGPYVSAKCSRIRDTVCATCAENS	60
QY	61 YNEHHWNYLTYCQLCPRCPDPVMGLHLRHAAPCTSKRKTCRQCPGMRCAAWALECTCIELSD	120
Db	61 YNEHHWNYLTYCQLCPRCPDPVMGLHLRHAAPCTSKRKTCRQCPGMRCAAWALECTCIELSD	120
QY	121 CPPGTAELKDEVKGKNNHCPKAGHFONTSSPARCOPHTRCNQGLYEAAPGTAQSD	180
Db	121 CPPGTAELKDEVKGKNNHCPKAGHFONTSSPARCOPHTRCNQGLYEAAPGTAQSD	180

Query Match	Score	DB	Length
Best Local Similarity	100.0%	1	197
Conservative	100.0%	1e-76	0
Matches	Mismatches	Indels	Gaps
QY	1	SOPQAVPPYASENQTCRDOKEVYEPORHICCSRCPGTYVSAKCSRIRDTCATTAENS	60
Db	1	SQPQAQVPPYASENQTCRDOKEVYEPQRHICCSRCPGTYVSAKCSRIRDTCATTAENS	60
QY	61	YNHHWWNYLTICOLCRPCDPVMGLEETAPCTSKEKTOCRQCOPGMFCIAWALECTCCEIISD	120
Db	61	YNEHHWWNYLTICOLCRPCDPVMGLEELIAPTSKRKTQCRQCOPGMFCIAWALECTCCEIISD	120
QY	121	CPPGTEALKDEYGKGNNHCVPKAGHFRONTSPSACOPHRCCENOCIVEAAGPTAQSD	180
Db	121	CPPGTEALKDEVGKGNNHCVPKAGHFRONTSPSACOPHRCCENOCIVEAAGPTAQSD	180
QY	181	TTCKNPPLPPLPPEMSGT	197
Db	181	TTCKNPPLPPLPPEMSGT	197

RESULT 2  
 ID AAY31325  
 AC XX  
 AC XX  
 DT 04-OCT-1999 (first entry)  
 DE Human lymphotxin (LT)beta-receptor extracellular region.  
 XX  
 KW Lymphotxin-beta; LT-beta; LT-beta receptor; follicular dendritic cell;  
 immune system; tumour; follicular lymphoma; extracellular domain; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9338525-A1.  
 XX  
 PD 05-AUG-1999.  
 XX  
 PR 29-JUN-1999; 99WO-US001928.  
 XX  
 PR 30-JUN-1998; 98US-0073112P.  
 PR 02-FEB-1998; 98US-0073410P.  
 XX  
 PA (BIOL ) BIOPHARMA INC.  
 XX  
 PI Browning J, Thorbecke J, Tsiaigbe V;  
 XX  
 DR PT  
 PT New method of treating follicular lymphomas by inhibiting interaction  
 between lymphotxin-beta and its receptor.  
 XX  
 PS Example 1; Page 25-26; 31PP; English.  
 CC The invention provides a method for arresting or reducing, severity of  
 effects of a tumour by administration of a composition which inhibits the

DE Human TNF receptor 2 related protein/LTRbeta SEQ ID NO:19.  
 XX  
 KW Human; tumour necrosis factor receptor 2 related protein variant;  
 KW TNFR2PV; cytostatic; immunosuppressive; antiasthmatic; gene therapy;  
 KW TNF signalling; cancer; inflammatory disorder; rheumatoid arthritis;  
 KW asthma; ulcerative colitis.  
 XX OS Homo sapiens.  
 XX PN WO2003012037-A2.  
 XX PD 13-FEB-2003.  
 XX PR 24-JUL-2002; 2002WO-US023684.  
 XX PR 27-JUL-2001; 2001US-00917372.  
 XX PA (INCYT-) INCYTE GENOMICS INC.  
 XX PI Lal PG, Warren BA;  
 XX DR WPI; 2003-256445/25.  
 XX PT New cDNA, useful for preparing a composition for treating a disease or  
 PT condition associated with increased TNF signaling e.g., cancer of the  
 prostate, ovary, gallbladder, breast, brain, liver or colon, or  
 PT rheumatoid arthritis, asthma.  
 XX Disclosure; Fig 2A-C; 64pp; English.  
 PS The present invention describes human tumour necrosis factor receptor 2  
 CC related protein variant (TNFR2PV). TNFR2PV has cytostatic, antiasthmatic

CC and immunosuppressive activities, and can be used in gene therapy. The TNFRPV cDNA or protein sequences can be used for preparing a composition for treating a disease or condition associated with increased TNF signalling e.g., cancer of the prostate, ovary, gallbladder, breast, brain, liver or colon, or inflammatory disorders, such as rheumatoid arthritis, asthma or ulcerative colitis. The present sequence represents a human TNFR2 related protein/lubeta amino acid sequence, which is given in comparison with human TNFRPV in the exemplification of the present invention.

XX SQ Sequence 435 AA;

Query Match	100.0%	Score	1133	DB	6	Length	435;
Best Local Similarity	100.0%	Pred.	No.	2	.3e-78;	Gaps	0;
Matches	197;	Conservative	0;	Mismatches	0;	Indels	0;
QY	1	SQPQAVPPYASENQTCRQDEKEYYEPQRHICCSRCRCPGTVSAKCSRIRDTVCATCAENS	60				
Db	28	SQPQAVPPYASENQTCRQDEKEYYEPQRHICCSRCRCPGTVSAKCSRIRDTVCATCAENS	87				
QY	61	YNEHWMLYTICOLCRCPDPMGLEELAPCTSKRKTOCRQCPGMFCRAWALECTHELLSD	120				
Db	88	YNEHWMLYTICOLCRCPDPMGLEELAPCTSKRKTOCRQCPGMFCRAWALECTHELLSD	147				
QY	121	CPPGTAEELKDEVGKGNNHCUPCKAGHFQNTSSPSARCOPHTRCENQGLVEAAPTQSD	180				
Db	148	CPPGTAEELKDEVGKGNNHCUPCKAGHFQNTSSPSARCOPHTRCENQGLVEAAPTQSD	207				
QY	181	TTCKNPLEPLPPENSGT	197				
Db	208	TTCKNPLEPLPPENSGT	224				

RESULT 4

ID	ABR40220	standard; protein; 435 AA.
XX	XX	ABR40220;
DT	12-JUN-2003	(first entry)
XX	XX	Human genoxin.
XX	XX	Human; genoxin; antiarteriosclerotic; antidiabetic; hypotensive; antilipemic; anorectic; immunomodulator; cytostatic; anti-HIV; antiinflammatory; antifibrinolytic; cardiotonic; cerebroprotective; gene therapy; antineoplastic; antitumour necrosis factor receptor; TNFR; body mass; weight loss; obesity.
OS	OS	Homo sapiens.
XX	XX	Key
FT	FT	Location/Qualifiers
FT	FT	1..30
FT	FT	/label= Signal_peptide
FT	FT	31..435
FT	FT	/label= Mature_genoxin
FT	FT	Domain
FT	FT	1..227
FT	FT	/label= Extracellular_domain
FT	FT	228..248
FT	FT	/label= Transmembrane_domain
FT	FT	249..435
FT	FT	/label= Intracellular_domain
XX	XX	WO2003011322-A1.
PN	XX	13-FEB-2003.
PF	XX	31-JUL-2002; 2002WO-IB003417.
PR	XX	02-AUG-2001; 2001US-0309917P.
PA	XX	(GEST ) GENSET SA.
PI	XX	Lucas J, Dialynas D, Briggs K;

XX DR WPI; 2003-256417/25.

XX N-PSDB; ABZ99578.

XX PT Screening for an agonist or antagonist of Genoxin activity, useful for preventing or treating metabolic disorders, comprising contacting Genoxin polypeptide with a test compound and determining binding.

XX PS Example 10; Page 33-34; 37pp; English.

XX SQ Sequence 435 AA;

Query Match	100.0%	Score	1133	DB	6	Length	435;
Best Local Similarity	100.0%	Pred.	No.	2	.3e-78;	Gaps	0;
Matches	197;	Conservative	0;	Mismatches	0;	Indels	0;
QY	1	SQPQAVPPYASENQTCRQDEKEYYEPQRHICCSRCRCPGTVSAKCSRIRDTVCATCAENS	60				
Db	28	SQPQAVPPYASENQTCRQDEKEYYEPQRHICCSRCRCPGTVSAKCSRIRDTVCATCAENS	87				
QY	61	YNEHWMLYTICOLCRCPDPMGLEELAPCTSKRKTOCRQCPGMFCRAWALECTHELLSD	120				
Db	88	YNEHWMLYTICOLCRCPDPMGLEELAPCTSKRKTOCRQCPGMFCRAWALECTHELLSD	147				
QY	121	CPPGTAEELKDEVGKGNNHCUPCKAGHFQNTSSPSARCOPHTRCENQGLVEAAPTQSD	180				
Db	148	CPPGTAEELKDEVGKGNNHCUPCKAGHFQNTSSPSARCOPHTRCENQGLVEAAPTQSD	207				
QY	181	TTCKNPLEPLPPENSGT	197				
Db	208	TTCKNPLEPLPPENSGT	224				

RESULT 5

ID	ABU9821	standard; protein; 435 AA.
XX	XX	ABU9821;
XX	XX	10-JUL-2003 (first entry)
XX	XX	TNF-receptor associated factor 5 (TRAF5) interacting protein #1.
XX	XX	Human; cytostatic; DAK3-Agonist; DAK3-An antagonist; cancer; TNF-receptor associated factor 5 interacting protein; tumour necrosis factor associated factor 5 interacting protein; TRAF5 interacting protein.
XX	XX	Homo sapiens.
XX	XX	WO2003031571-A2.
PD	XX	17-APR-2003.

PF 02-OCT-2002; 2002WO-US031357.  
 XX KN Human; tumour necrosis factor receptor 2 related protein variant;  
 PR TNFR2P; cytostatic; immunosuppressive; antiasthmatic; gene therapy;  
 PR KW TNF signalling; cancer; inflammatory disorder; rheumatoid arthritis;  
 PR asthma; ulcerative colitis;  
 PR XX OS Homo sapiens.  
 PR XX PN WO200312037-A2.  
 PR XX PD 13-FEB-2003.  
 PR XX XX 29-OCT-2001; 2001US-0349575P.  
 PR XX PF 01-NOV-2001; 2001US-0346357P.  
 PR XX PR 25-JUN-2002; 2002US-0391342P.  
 PR XX PR 01-OCT-2002; 2002US-00262445.  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PT Alsobrook JP, Burgess CE, Catterton E, Chant JS, Chaudhuri A;  
 PT Edinger SR, Gerlach VL, Giot L, Gorman L, Guo X, Kekuda R;  
 PI Mezes PS, Millet I, Ooi CE, Paturajan M, Rieger DK, Spytek KA;  
 PT Taupier RJ, Zernhusen BD, Zhong H, Zhong M;  
 XX WPI: 2003-381704/36.  
 DR N-PSDB; ACA9237.

XX  
 PT New DAPK3 polypeptide, useful for preparing a composition for treating or preventing e.g., cancer.  
 PT preventing e.g., cancer.  
 XX  
 PS Example 20F; Page 240; 253pp; English.  
 XX  
 CC The invention describes an isolated polypeptide comprising any of 33 90-  
 CC 1273 amino acid sequences (1) given in the specification or its mature  
 CC form, a sequence that is at least 95 % identical to (1), or a sequence  
 CC comprising one or more conservative substitutions in the amino acid  
 sequence of (1). The polypeptide is useful for preparing a composition  
 CC for treating or preventing e.g. cancer. This is the amino acid sequence  
 CC of a tumour necrosis factor (TNF)-receptor associated factor 5 (TRAF5)  
 CC interacting protein associated with the identification of novel human  
 CC proteins and their functions  
 XX  
 SQ Sequence 435 AA;

Query Match	Score	DB	Length
Best Local Similarity	100.0%	6	435;
Matches	100.0%	Pred. No.	2.3e-78;
	0;	Indels	0;
		Gaps	0;

QY 1 SQPQAVPPYASENQTCRQEPGYEYQHRCICSRCPGTVYSAKSRSRIRTVCATCAENS 60  
 Db 28 SQPQAVPPYASENQTCRQEPGYEYQHRCICSRCPGTVYSAKSRSRIRTVCATCAENS 87  
 QY 61 YNEHWMLTICOLCRCPDPVNGLEELAPCTSSKRKTQCRCPGMFC2AAWALECTHCBLLSD 120  
 Db 88 YNEHWMLTICOLCRCPDPVNGLEELAPCTSSKRKTQCRCPGMFC2AAWALECTHCBLLSD 147  
 QY 88 YNEHWMLTICOLCRCPDPVNGLEELAPCTSSKRKTQCRCPGMFC2AAWALECTHCBLLSD 147  
 Db 121 CPPGTEAKLDEVGKGNHCVCKAGHFQNTSSSPARCQPHRCENQGLVRAAPGTAQSD 180  
 QY 148 CPPGTEAKLDEVGKGNHCVCKAGHFQNTSSSPARCQPHRCENQGLVRAAPGTAQSD 207  
 QY 181 TTCKNPFLPEPLPPEMSGT 197  
 Db 208 TTCKNPFLPEPLPPEMSGT 224

SQ Sequence 399 AA;

Query Match	Score	DB	Length
Best Local Similarity	99.5%	6	399;
Matches	196;	Conservative	1;
		Mismatches	0;
		Indels	0;
		Gaps	0;

QY 1 SQPQAVPPYASENQTCRQEPGYEYQHRCICSRCPGTVYSAKSRSRIRTVCATCAENS 60  
 Db 28 SQPQAVPPYASENQTCRQEPGYEYQHRCICSRCPGTVYSAKSRSRIRTVCATCAENS 87  
 QY 61 YNEHWMLTICOLCRCPDPVNGLEELAPCTSSKRKTQCRCPGMFC2AAWALECTHCBLLSD 120  
 Db 88 YNEHWMLTICOLCRCPDPVNGLEELAPCTSSKRKTQCRCPGMFC2AAWALECTHCBLLSD 147  
 QY 121 CPPGTEAKLDEVGKGNHCVCKAGHFQNTSSSPARCQPHRCENQGLVRAAPGTAQSD 180  
 Db 148 CPPGTEAKLDEVGKGNHCVCKAGHFQNTSSSPARCQPHRCENQGLVRAAPGTAQSD 207  
 QY 181 TTCKNPFLPEPLPPEMSGT 197  
 Db 208 TTCKNPFLPEPLPPEMSGT 224

RESULT 7

ID ADC42856 standard; protein; 416 AA.  
 ID ADC42856  
 XX AC ADC42856;  
 XX DT 18-DEC-2003 (first entry)  
 DE REMAP protein #16.  
 XX KW Cytostatic; Antiarteriosclerotic; Anti-HIV; Antinflammatory;  
 DE Human TNF receptor 2 related protein variant SEQ ID NO:1.

RESULT 6

ID ABP96136 standard; protein; 399 AA.  
 ID ABP96136  
 XX AC ABP96136;  
 XX DT 09-MAY-2003 (first entry)  
 DE Human TNF receptor 2 related protein variant SEQ ID NO:1.

KW Antiallergic; Antidiabetic; REMAP; pathogenesis.  
 XX  
 OS Homo sapiens.

XX  
 WO2003027228-A2.

PD 03-APR-2003.

XX  
 FF 16-JUL-2002; 2002WO-US022833.

XX  
 PR 17-JUL-2001; 2001US-0306020P.

PR 27-JUL-2001; 2001US-0308179P.

PR 02-AUG-2001; 2001US-0303702P.

PR 10-AUG-2001; 2001US-0311476P.

PR 10-AUG-2001; 2001US-0311551P.

PR 24-AUG-2001; 2001US-0311718P.

PR 31-AUG-2001; 2001US-0314798P.

PR 07-SEP-2001; 2001US-0317996P.

PA (INCYT) INCYTE GENOMICS INC.

XX  
 PI Lal PG, Honchell CD, Forsythe IJ, Walia NK, Tang TY, Borowsky ML;

PI Barroso I, Yue H, Warren BA, Thangavelu K, Gietzen KJ, Azmzai Y;

PI Lee EA, Baughn MR, Gorvad AB, Duggan BM, Tran B, Li JX;

PI Richardson TW, Elliott VS, Zebardadian Y, Tran UK, Yao MG;

PI Peterson DP, Luo W, Lehr-Mason PM;

XX  
 DR WPI; 2003-421156/39.

XX  
 PT New human receptors and membrane-associated proteins (REMAP), useful for

PT preventing, treating or preventing disorders associated with aberrant or

PT REMAP expression, e.g. cancer, AIDS, atherosclerosis, hypertension or

PT stroke.

XX  
 PS Claim 1; SEQ ID NO 16; 115pp; English.

The present invention relates to an isolated polypeptide. The polyPeptides and polynucleotides are useful in diagnosing, treating and preventing disorders associated with aberrant expression of REMAP, such as cell proliferative, autoimmune/inflammatory, renal, neurological, cardiovascular, metabolic, developmental, endocrine, muscle, gastrointestinal, lipid metabolism or transport disorders, and viral infections. These are also useful in assessing the effects of exogenous compounds on the expression of nucleic acids and amino acid sequences of REMAP, in facilitating drug discovery process, and in investigating the pathogenesis of diseases or medical conditions. Expression and purification were achieved using bacterial or virus-based expression systems. The present sequence represents an REMAP protein of the CC invention.

XX  
 SQ Sequence 416 AA;

Query Match 97.8%; Score 1108; DB 7; Length 416;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-76; Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VPPYASENQTCRDQEKEYEYEPQRHICCSRCGPGLTVSAKCSRIRDTVCACTAENSYNEW 65  
 Db 14 VPPYASENQTCRDQEKEYEYEPQRHICCSRCGPGLTVSAKCSRIRDTVCACTAENSYNEW 73

Qy 6 NYLTICOLCRCPDPVGLEELAPCTSKRKHQCRGFCRAWALECTHELLSDCPGT 125  
 Db 74 NYLTICOLCRCPDPVGLEELAPCTSKRKHQCRGFCRAWALECTHELLSDCPGT 133

Qy 126 EAEIKDEVGKNNHYPCKAGHFQNTSSSARCOPHTRFENQLVAACTAQSDTICK 185  
 Db 134 EAEIKDEVGKNNHYPCKAGHFQNTSSSARCOPHTRFENQLVAACTAQSDTICK 193

Qy 186 PLEPIPPEMSGT 197  
 Db 194 PLEPIPPEMSGT 205

RESULT 8

ADA49700

ID ADA49700 standard; protein; 170 AA.

XX  
 AC ADA49700;

XX  
 DT 20-NOV-2003 (first entry)

XX  
 DE Extracellular region of human TNFRrp (htNFRrp) protein.

XX  
 KW Apo-2 ligand inhibitor; Apo-2LI; Apo-3; apoptosis; affinity; competitive-type receptor; binding assay; cancer cell; human; TNF receptor family; hTNFRrp; cytostatic.

XX  
 OS Homo sapiens.

XX  
 PN US2002192729-A1.

XX  
 PD 19-DEC-2002.

XX  
 PF 28-MAR-2002; 2002US-00112793.

XX  
 PR 01-APR-1996; 96US-00615328.

PR 23-SEP-1996; 96US-00710802.

PR 31-MAR-1997; 97US-00828683.

PA (GETH ) GENENTECH INC.

XX  
 PI Ashkenazi AJ;

XX  
 DR WPI; 2003-657226/62.

XX  
 PT Novel isolated biologically active Apo-2 ligand inhibitor polypeptide, or

PT Apo-3 polypeptide which induces or stimulates apoptotic activity, useful in diagnostic assays.

XX  
 PS Disclosure; Fig 2; 53pp; English.

XX  
 CC The present invention relates to the isolation of a biologically active

CC Apo-2 ligand inhibitor (Apo-2LI) or Apo-3, and the polynucleotide

CC sequences encoding them. Apo-2LI and Apo-3 are involved in apoptosis. The

CC Apo-2LI and Apo-3 polypeptides are useful in diagnostic assays. Apo-2LI

CC is useful for generating antibodies, as standards in assays for Apo-3 or

CC Apo-2LI, in affinity purification techniques, and in competitive-type

CC receptor binding assays when labelled with radiiodine, enzymes or

CC fluorophores. Agonistic Apo-3 antibodies are useful for stimulating or

CC inducing apoptosis in cancer cells, and thus have therapeutic utility.

CC The present sequence represents the extracellular region of a human TNF

CC receptor family protein. This sequence is compared with the extracellular

CC region of human Apo-2LI.

XX  
 SQ Sequence 170 AA;

Query Match 87.1%; Score 987; DB 6; Length 170;

Best Local Similarity 100.0%; Pred. No. 1.2e-67; Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TCRDQEKEYEYEPQRHICCSRCGPGLTVSAKCSRIRDTVCACTAENSYNEW 74  
 Db 1 TCRDQEKEYEYEPQRHICCSRCGPGLTVSAKCSRIRDTVCACTAENSYNEHWNLYTICOLC 60

Qy 75 RPCDPMVGLEELAPCTSKRKHQCRGFCRAWALECTHELLSDCPGT 134  
 Db 61 RPCDPMVGLEELAPCTSKRKHQCRGFCRAWALECTHELLSDCPGT 120

Qy 135 KGNNHCVPCKAGHFQNTSSSARCOPHTRFENQLVAACTAQSDTICK 184  
 Db 121 KGNNHCVPCKAGHFQNTSSSARCOPHTRFENQLVAACTAQSDTICK 170

RESULT 9  
 AAB36700

				AAB36700; 15-MAR-2001 (first entry)	XX Human tumour necrosis factor receptor TRID protein SEQ ID NO:6.
AC					KW Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; nontropic; TRAIL receptor without intracellular domain; diagnosis; cytostatic; tumour necrosis factor related apoptosis inducing ligand; vasoconstrictive; immunosuppressive; neuroprotective; antiviral; antiinflammatory; anti-convulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian; gene therapy; restenosis; graft versus host disease; tumour; cancer; apoptotic cell death related disease; autoimmune disorder; cardiovascular disorder; viral infection.
DE					KW Homo sapiens.
XX					OS
PN					PN WO200071150-A1.
XX					PD 30-NOV-2000.
XX					PT 18-MAY-2000; 2000WO-US013515.
XX					PR 20-MAY-1999; 99US-0135164P.
XX					PA (HUMA-) HUMAN GENOME SCI INC.
XX					PI Wei Y, Ruben SM, Gentz RL, Ni J;
XX					DR WPI; 2001-041051/05.
XX					PT Nucleic acid encoding a TRID polypeptide, also referred to as tumor necrosis factor receptor 5, useful in the diagnosis, treatment or prevention of cancer, autoimmune disorders and viral infection.
XX					PS Disclosure: Fig 2; 285PP; English.
CC					CC The present invention describes the human TRID protein (tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without intracellular domain, also referred to as tumour necrosis factor receptor 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive, nontropic, neuroprotective, antiviral, antiinflammatory, anticonvulsant, antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasoconstrictive activities, and can be used in gene therapy. The TRID polynucleotides are useful for detecting complementary polynucleotides. TRID proteins and polynucleotides are useful in the treatment of tumours, resistance to parasites, bacteria and viruses, restenosis. They are also useful for inducing proliferation of T-cells, endothelial cells and certain haemopoietic cells, to regulate antiviral responses and to prevent certain autoimmune diseases after stimulation of TRID by an agonist or TRAIL binding facilitator. The antibodies which bind TRID polypeptides are useful for treating and/or preventing diseases associated with increased or decreased apoptotic cell death. The TRID polynucleotides, proteins, antibodies, agonists and antagonists are useful in the diagnosis, treatment or prevention of: (a) cancer; (b) autoimmune disorders; (c) diseases associated with increased apoptosis; (d) cardiovascular disorders; and (e) viral infection. The present sequence represents a tumour necrosis receptor used in comparison with TRID in the exemplification of the present invention
CC					CC Sequence 415 AA;
SQ					Query Match 68.0%; Score 771; DB 4; Length 415; Best Local Similarity 70.7%; Pred. No. 8.4e-51; Mismatches 135; Conservative 14; Indels 2; Gaps 1;
QY					1 SQPQAVPYASENQTCRDKQEKEYEPHRICCSRCPGTYVSAKCSRIRDYVCAENS 60
Db					28 SQPQLVPYRINTQTCWQDKQEKEYEPHMHDVCCSRCSRCPGPFRFVAVCSRSQDVTCKTCPHNS 87
QY					61 YNHHWNYLITCQLCRPCDPVMGLEELIADPTSKERKTQCRQGMHECAAWELETHC-BLL 118

Db 8 YNEHHWHLSTCQLCRPCDIDVLFEEVAPCTSDRKAECCRQPGMSCVLNDNECVHCEERL 147  
 Qy 119 SDCPPTETEAEKLDEVGKGNHCVPKCAGFQNTSSPASRQPHTCENQGILVEAARGTAQ 178  
 Db 148 VLQQPRTETAEVTDIDMDTVDNCVCPKGPFRONTSSRACRQPHTCIQSILVERAAGFTSY 207  
 Qy 179 SDTICKNPLEP 189  
 Db 208 SDTICKNPEP 218

RESULT 11  
 AAW94642  
 ID AAW94642 standard; peptide; 77 AA.  
 XX  
 AC AAW94642;  
 XX  
 DT 29-APR-1999 (first entry)  
 XX  
 TNF-R extracellular Cys-rich domain TNF-R-RP.  
 Tumour necrosis factor receptor; TNF-R; autoimmune diseases; KW  
 inflammation; septic shock; cachexia; graft versus host disease; KW  
 skin allergic reaction; immune complex disease; malaria; KW  
 transplantation rejection.  
 XX  
 OS Homo sapiens.  
 XX  
 WO9853842-A1.  
 XX  
 PD 03-DEC-1998.  
 XX  
 PP 29-MAY-1998; 98WO-US010891.  
 XX  
 PR 30-MAY-1997; 97US-00866545.  
 XX  
 (UYPE-) UNIV PENNSYLVANIA.  
 PA Greene MI, Murali R, Takasaki W;  
 XX  
 PI DR  
 XX  
 WPI; 1999-080781/07.  
 XX  
 PT New compounds designed from a binding loop of a tumour necrosis factor receptor - are capable of inhibiting the biological activities of tumour necrosis factor, e.g., in treating inflammation or autoimmune diseases.  
 XX  
 PS Disclosure; Fig 1; 78pp; English.  
 XX  
 CC The present invention describes peptides and peptide analogues which correspond in primary sequence to a binding loop of a tumour necrosis factor receptor (TNF-R) superfamily member. The compounds are especially designed from a binding loop of TNF-R p55. They are capable of inhibiting TNF binding to its cellular receptors and may be used to inhibit the biological activities of TNF. They may be used in treating TNF-associated conditions such as acute and chronic inflammatory responses, septic shock, cachexia, autoimmunity, graft-versus-host disease, skin allergic reactions, immune complex disease, transplantation rejection and malaria. Administration is, e.g. oral, transdermal, pulmonary, subcutaneous, intravenous or intramuscular. Parenteral dosage is 0.1-5 mg/kg/day. The present sequence represents an extracellular Cys-rich domain of TNF-R from the present invention  
 CC domain of TNF-R from the present invention  
 XX  
 SQ Sequence 77 AA;

Query Match 40.2%; Score 456; DB 2; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-27;  
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 VCATCAENSNHWNLYTICOLCRPCDPVMGLEEAPCTSKRKTOCRQGMFCAWALE 111  
 Db 1 VCATCAENSNHWNLYTICOLCRPCDPVMGLEEAPCTSKRKTOCRQGMFCAWALE 60

Db 112 CTHCEILSDCOPPGTAE 128  
 Qy 61 CTHCEILSDCOPPGTAE 77  
 Db RESULT 12  
 AAB69194  
 ID AAB69194 standard; protein; 77 AA.  
 XX  
 AC AAB69194;  
 XX  
 DT 30-APR-2001 (first entry)  
 XX  
 DE Human TNF-R extracellular Cys-rich domain TNF-R-RP SEQ ID NO:3.  
 XX  
 KW Tumour necrosis factor receptor; TNF-R; inhibition; osteoclast; KW  
 osteoclastogenesis; bone loss; bone resorption; osteopathic; cytoprotective; KW  
 anti-rheumatic; antiarthritic; antiinflammatory; immunomodulatory; KW  
 tumour necrosis factor-related activation-induced cytokine; TRANCE; KW  
 receptor activator of NF-kappaB ligand; RANK; osteoprosis; KW  
 Paget's disease; metastatic bone disease; rheumatoid arthritis; KW  
 periodontal disease; modulating dendritic cell maturation; KW  
 T cell proliferation; CD40 receptor system.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200108699-A1.  
 XX  
 PD 08-FEB-2001.  
 XX  
 PP 28-JUL-2000; 2000WO-US020510.  
 XX  
 PR 28-JUL-1999; 99US-0146090P.  
 XX  
 PA (UYPE-) UNIV PENNSYLVANIA.  
 PA (AOKI/) AOKI K.  
 PA (HORNE/) HORNE W C.  
 PA (BARON/) BARON R.  
 XX  
 Aoki K, Horne WC, Baron R, Greene MI, Murali R;  
 XX  
 PI DR  
 XX  
 WPI; 2001-18266/18.

PT Use of peptides and peptide analogs which are TRANCE/RANK inhibitors, for PT  
 inhibiting osteoclastogenesis and bone resorption.  
 XX  
 PS Disclosure; Fig 1; 81pp; English.

XX  
 CC The present invention describes a method for inhibiting osteoclastogenesis and bone resorption. Osteoclastogenesis and bone resorption inhibiting peptide analogues from the present invention have osteopathic, cytostatic, anti-rheumatic, antiarthritic, antiinflammatory and immunomodulatory activities, and are tumour necrosis factor (TNF)-related activation-induced cytokine (TRANCE)/receptor activator of NF-CC kappaB ligand (RANK) inhibitors. The method is useful for treating CC diseases characterised by bone loss such as osteoporosis, Paget's CC disease, metastatic bone disease, rheumatoid arthritis or periodontal CC disease, and modulating dendritic cell maturation, T cell proliferation, and/or CD40 receptor systems. The present sequence represents an extracellular Cys-rich domain of a tumour necrosis factor receptor (TNF-CC) superfamily member, which is used in the exemplification of the present invention  
 XX  
 SQ Sequence 77 AA;

Query Match 40.2%; Score 456; DB 4; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-27;  
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 VCATCAENSNHWNLYTICOLCRPCDPVMGLEEAPCTSKRKTOCRQGMFCAWALE 111  
 Db 1 VCATCAENSNHWNLYTICOLCRPCDPVMGLEEAPCTSKRKTOCRQGMFCAWALE 60

Qy 112 CTHCELLSPCPGTEAE 128  
 ||||| ||||| |||||  
 61 CTICBLLSDCPGTEAE 77

RESULT 13

ABP41926

XX

AC ABP41926;

XX

DT 22-AUG-2002 (first entry)

XX

DE Human ovarian antigen HSABU44, SEQ ID NO:3058.

XX

KW ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; chromosome 12p13.

KW XX

OS Homo sapiens.

OS XX

PN WO200200677-A1.

XX

PD 03-JAN-2002.

XX

PF 07-JUN-2001; 2001WO-US018569.

XX

PR 07-JUN-2000; 2000US-0209467P.

XX

PA (HOMA-) HUMAN GENOME SCI INC.

XX

PI Birse CE, Rosen CA;

XX

DR WPI; 2002-147878/19.

XX

PS Claim 11; SEQ ID NO 3058; 2922pp; English.

XX

CC

the Fc portion of human IgG1. Plasmid pIXX498 is a yeast expression vector contg. the Fc fragment of human IgG1. 3) An oligo linker, to fuse the truncated TNFR with the human IgG1 Fc fragment. This linker was created by PCR using primer ARQ45226, which encodes the 3' end of the truncated TNF receptor and the 5' end of human IgG1, and primer AQ45227, which is an antisense sequence encoding bps 257-237 of human IgG1. (Updated on 25-MAR-2003 to correct PN field.)

CC soluble domain or a different soluble domain of a biologically active protein. The methods and compositions of the present invention are useful for the diagnosis and treatment of disorders associated with dimeric protein or its glycosylated form, such as inflammation, septicemia, cytotoxicity, rheumatoid arthritis, cachexia and other inflammatory-related diseases. This sequence represents the human concatameric protein of the invention.

Query Match	Best Local Similarity	Score	DB	Length
Matches	35.5%	315	2	518
	Conservative	5	9e-16	
		Mismatches	Indels	Gaps
Y	AVPPVASE-NQCPQRDCDQEKEYPQRHICCSRSPPGTVSAKCSRIRIPTVACATCAENSYNE	5	37	9
b	AFTPYAEPGSGCR-IKEYYDQTAQMCCKSKSPGQAKVFCTKTSTVUCSDSYTQ	57	11	1
Y	HWNLYLTICQLCR--PDDPVMGLEETAPCTSRRKTTQRCQPSGMFCAAWALE-CTHCELLS	64	119	1
b	IWNWVPHCLSCGSRCSDQV---ETQACTREBQNRTCTCPRGWYCALSKQBGCRLLCAPR	115	170	1
Y	DCPPG----TEAELXDEVKGKNNHCYCKPCKACHFQNTSSPSARCQPIRCECENOGLVIAAP	120	174	1
b	KORPGGGVARPGTETSPVY-----CRPCAPGTFSNTTSSIDICRPHQICN----VVAIP	171	220	1
Y	GTAQSPTTC- KNPLELPP	175	192	1
b	GNASMDAVCTISSPTRSMAP	221	240	1

Query	Match	Score	Length
Best Local Similarity	27.5%	311.5	659
Matches 71; Conservative	Pred. No.	1.4e-15	
Mismatches 23;	Indels	27	
Matches 71;	Gaps		9
Qy 5 AVPPYASS-NQCRDQEKEYYEPOHRTICCSRCPGTTIVYSAKCSIRDTCATCARNSYNE	63		
Db 28 AFMPPYAPPERGSTOR--LIREYDQTAMQCSCSKCSQHQAKFVPTKNSDVTCDSESYTQ	85		
Qy 64 HWWYLITICOLCR--PCDPVMGLEBIAPICTSRSRKTCRQCRQGMCCAAWALE-CTHCELLS	119		
Db 86 LWWWWPBCISCGSRSQSDQV---ETQACTREPDRCRTPGMWCAALSKOEGCRICAPL	141		
Qy 120 DCPFG-----TEABLKDEVGKGNNHCVPCCKAGHQNTISPSARQPHTRGENQIGVEAAP	174		
Db 142 KCRPGFGVARPGTETSDVV-----CKPCAPGTFSTSSTDICRPHQION---WVAIP	191		
Qy 175 GTAQSDTICKNPKIPEP	189		
Db 192 GNASMDANCTSP-EP	205		

RESULT 15

Search completed: August 28, 2004, 01:47:03  
Job time : 129 secs

ABU37103;  
08-MAY-2003 (first entry)  
Concattameric immunoadhesion human protein sequence SEQ ID No 12.  
Antiflammatory; antibacterial; immunosuppressive; anti rheumatic;  
antiarthritic; immunomodulator; concattameric protein; soluble domain;  
dimeric protein; inflammation; septicaemia; cytotoxicity;  
rheumatoid arthritis; cachexia; inflammation; human.  
Homo sapiens.

WO2003016202-A1.  
06-FEB-2003.  
26-JUL-2002; 2002WO-KR001427.  
26-JUL-2001; 2001KR-00045028.  
(MEDB-) MEDEXGEN CO LTD.  
Chung Y, Han J, Lee H, Choi E, Kim J;  
WPI; 2003-229639/22.  
N-PSDB; ABT32046.

T New concatameric protein having two soluble domains, useful for  
T diagnosing and treating disorders associated with the dimeric protein  
T its glycosylated form, such as inflammation, septicemia, rheumatoid  
T arthritis and cachexia.

X Claim 27; Page 148-152; 211pp; English.

S

C The invention relates to a novel concatameric protein comprising two  
C soluble domains, in which an N-terminus of a soluble domain of a  
biologically active protein is linked to a C-terminus of an identical

T



GenCore version 5.1.6  
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### OM protein - protein search, using sw model

Run on: August 28, 2004, 01:43:28 ; Search time 40 Seconds

Sequence: 1 SQPQAVPPYASENQTCRDQE.....QSDTCKNPLEPLPPEMSGT 197

Title: US-10-003-211-1  
Perfect score: 1133  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR\_78:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	1133	100.0	435	2	I54182 tumor necrosis factor receptor 2-related protein - human
2	305	26.9	461	1	A35356 tumor necrosis fac
3	295	26.0	474	2	B38634 tumor necrosis fac
4	290	25.6	459	2	I48854 gene murine tumour
5	278	24.5	277	2	A60771 B-cell activation
6	243	21.5	305	2	A46476 B cell-associated
7	226	20.0	651	2	JC7705 death receptor-6 -
8	222	19.6	271	2	S12783 OX40 antigen precu
9	19	18.9	272	2	I48700 gene ox40 protein
10	210.5	18.6	455	1	Q0HUT1 tumor necrosis fac
11	210	18.5	348	2	T28623 hypothetical prote
12	210	18.5	349	2	D36858 gene G4R protein -
13	207	18.3	349	2	D72175 G2R protein - vari
14	206	18.2	461	2	JC4302 tumor necrosis fac
15	201	17.7	277	2	OX40 homolog - hum
16	201	17.7	454	1	Q0MST1 tumor necrosis fac
17	196	17.3	595	2	A42086 CD30 antigen precu
18	195	17.3	255	2	Lymphocyte activat
19	189	16.7	325	2	T2 protein - rabbi
20	187.5	16.5	314	2	FAS soluble protei
21	184.5	16.3	461	1	tumor necrosis fac
22	183.5	16.2	326	1	GQVZML T2 protein - mycom
23	181	16.0	335	2	A4036 tumor necrosis factor receptor 2 precursor [validated] - human
24	179.5	15.8	256	2	B32393 A35356 tumor necrosis factor receptor receptor 2 precursor [validated] - human
25	171.5	15.1	425	1	A26431 T-cell antigen 4-1
26	166	14.7	493	2	JCS486 membrane glycoprot
27	164	14.5	416	1	NC0006 nerve growth facto
28	162	14.3	327	2	A46484 apoptosis-mediati
29	148.5	13.1	427	1	GOFUN nerve growth facto

RESULT 1

154182 tumor necrosis factor receptor 2-related protein - human

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 17-Mar-2000

C;Accession: I54182 R;Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.

Genomics 16, 214-218, 1993

A;Title: Construction and evaluation of a hmcDNA library of human 12p transcribed sequ

A;Reference number: I54182; PMID:93252381; PMID:8486360

A;Accession: I54182

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: mRNA

A;Residues: 1-435 <RES>

A;Cross-references: GDB:1230195; OMIM:600979

A;Gene: GDB:LTR

A;Map position: 12p13.3-12p13.1

C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match Local Similarity 100.0%; Score 1133; DB 2; Length 435; Best Local Similarity 100.0%; Score 1133; DB 2; Length 435; Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQPQAVPPYASENQTCRDQEKEYYPHQHRCCSRSPGTVSAKSRIRDTCATCAENS 60

Db 28 SQPQAVPPYASENQTCRDQEKEYYPHQHRCCSRSPGTVSAKSRIRDTCATCAENS 87

Qy 61 YNEHHWYLITICQLCPCDPGMLEIAPCTSKRKQCRCPGMFRRAWAELCTHELLSD 120

Db 61 YNEHHWYLITICQLCPCDPGMLEIAPCTSKRKQCRCPGMFRRAWAELCTHELLSD 147

Qy 88 YNEHHWYLITICQLCPCDPGMLEIAPCTSKRKQCRCPGMFRRAWAELCTHELLSD 147

Db 88 YNEHHWYLITICQLCPCDPGMLEIAPCTSKRKQCRCPGMFRRAWAELCTHELLSD 147

Qy 121 CPPGTAAELKDEVKGKNNHCPCAKHFQNTSSPARCOPHTRCENQGLVBAAPTAQSD 180

Db 121 CPPGTAAELKDEVKGKNNHCPCAKHFQNTSSPARCOPHTRCENQGLVBAAPTAQSD 180

Qy 148 CPPGTAAELKDEVKGKNNHCPCAKHFQNTSSPARCOPHTRCENQGLVBAAPTAQSD 207

Db 148 CPPGTAAELKDEVKGKNNHCPCAKHFQNTSSPARCOPHTRCENQGLVBAAPTAQSD 207

ALIGNMENTS

Fas antigen precur  
CD27 antigen precur  
hypothetical prote  
hypothetical prote  
laminin alpha-1 ch  
furan (EC 3.4.21.7  
cysteine rich prot  
laminin alpha 5 ch  
hypothetical prote  
subtilisin-like pr  
subtilisin-like pr  
heparan sulfate pr  
furan (EC 3.4.21.7  
Delta-4 protein -  
DETA-like 1 - mou  
subtilisin-like pr

A;Reference number: A35356; MUID:90260639; PMID:2160731  
A;Accession: A35356  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-461 <SMI>  
A;Cross-references: GB:M32315; NID:9189185; PIDN:AAA59929\_1; PID:9189186  
R;Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires, Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990  
A;Title: A second tumor necrosis factor receptor gene product can shed a naturally occur  
A;Reference number: A36475; MUID:91045991; PMID:2172983  
A;Accession: A36475  
A;Molecule type: mRNA  
A;Residues: 1-195, 'R', 197-461 <KOH>  
A;Cross-references: GB:M55994; GB:M38549; NID:9339757; PIDN:AAA36755\_1; PID:9339758  
R;Dembic, Z.; Loescher, H.; Gubler, U.; Pan, Y.C.; Lahn, H.W.; Gentz, R.; Brockhaus, M. Cytokine 2, 231-237, 1990  
A;Title: Two human TNF receptors have similar extracellular, but distinct intracellular, domains  
A;Reference number: A48416; MUID:91370690; PMID:1966549  
A;Accession: A48416  
A;Status: preliminary  
A;Molecule type: mRNA; Protein  
A;Residues: 23-461 <DEM>  
A;Cross-references: GB:S63368; NID:9235648; PIDN:ABR19824\_1; PID:9235649  
R;Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990  
A;Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration of its biological activity  
A;Reference number: A36007; MUID:90349572; PMID:2166546  
A;Accession: A36007  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 166-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEL>  
A;Cross-references: GB:M35857; NID:9339751; PIDN:AAA6262\_1; PID:9339752  
R;Loetscher, H.; Schlaeger, F.J.; Lahn, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M. J. Biol. Chem. 265, 20313-20318, 1990  
A;Title: Purification and partial amino acid sequence analysis of two distinct tumor necrosis factor receptors from human urine. Evidence for two distinct forms of the receptor  
A;Reference number: A23666; MUID:91056048; PMID:2173696  
A;Accession: A23666  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 23-40; 65-69; 136-141; 300-306 <LOE>  
R;Engelmann, H.; Novick, D.; Wallach, D.  
J. Biol. Chem. 265, 1531-1536, 1990  
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence for two distinct forms of the receptor  
A;Reference number: A35010; MUID:90110215; PMID:2153136  
A;Accession: B35010  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 27-31 <NG>  
R;Kuhner, P.; Kemper, O.; Wallach, D.  
Gene 150, 381-386, 1994  
A;Title: Cloning, sequencing and partial functional characterization of the 5' region of a mouse tumor necrosis factor receptor gene  
A;Reference number: 138034; MUID:95121934; PMID:7921811  
A;Accession: 138094  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 1-37 <RES>  
A;Cross-references: EMBL:X80021; NID:9666044; PIDN:CAA56324\_1; PID:9825701  
A;Genetics:  
A;Gene: GDB:TNFR2  
A;Cross-references: GDB:125914; OMIM:191191  
A;Introns: 26/3  
A;Note: the list of introns is incomplete  
C:Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolog  
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein  
C:Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolog  
C:Keywords: cytokine receptor; transmembrane protein  
F;1-22/Domain: signal sequence #status predicted <SIG>  
F;1-22/Domain: signal sequence #status predicted <SIG>  
F;23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>  
F;40-77/Domain: NGF receptor repeat homology <NG3>  
F;78-119/Domain: NGF receptor repeat homology <NG2>  
F;120-162/Domain: NGF receptor repeat homology <NG3>  
F;164-201/Domain: NGF receptor repeat homology <NG4>

Query Match 5 AVPYAS NOTCQDQEKEYEPQRICRCSRCPTIVNSAKCSRIRDDTVCAENSYHN Score 305; DB 1; Length 461; Best Local Similarity 35.0%; Pred. No. 6. 1e-15; Indels 78; Gaps 9; Matches 70; Conservative 24; Mismatches 119  
Query Match 5 AVPYAS NOTCQDQEKEYEPQRICRCSRCPTIVNSAKCSRIRDDTVCAENSYHN Score 305; DB 1; Length 461; Best Local Similarity 35.0%; Pred. No. 6. 1e-15; Indels 28; Gaps 9; Matches 70; Conservative 24; Mismatches 78; Gaps 9; Matches 70; Conservative 24; Mismatches 119  
QY 5 AVPYAS NOTCQDQEKEYEPQRICRCSRCPTIVNSAKCSRIRDDTVCAENSYHN Score 305; DB 1; Length 461; Best Local Similarity 35.0%; Pred. No. 6. 1e-15; Indels 28; Gaps 9; Matches 70; Conservative 24; Mismatches 78; Gaps 9; Matches 70; Conservative 24; Mismatches 119  
Db 28 AFTPYAPEPGSTCR--LRBYDQTAQMCCKSPQHAKVFCTKNSDTCSDCSDTYQ 141  
Db 28 AFTPYAPEPGSTCR--LRBYDQTAQMCCKSPQHAKVFCTKNSDTCSDCSDTYQ 141  
QY 120 DCPRG----TEAELKDENGKGNHCVPKAGHFONTSSPARCOPHTRCENQGLVEAP 174  
Db 142 KCRPGFGVARPGTETSDVV-----CKPCAGTSNTSSTDICRPHQION---WVAIP 191  
QY 175 GTAQSDTTC--KNPIEPLPP 192  
Db 192 GNASMDAVCTSTSPTRSMAP 211  
Db 192 GNASMDAVCTSTSPTRSMAP 211

RESULT 3  
B38634 tumor necrosis factor receptor type 2 precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text\_change 27-Oct-2003  
C;Accession: B3634; A40254; S54816  
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E. Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991  
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor A;Reference number: A38634; MUID:91187885; PMID:1849278  
A;Accession: B38634  
A;Molecule type: mRNA  
A;Residues: 1-474 <LEW>  
A;Cross-references: GB:M60469; NID:9199827; PIDN:AAA39752\_1; PID:9199828  
R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jen Mol. Cell. Biol. 11, 3020-3026, 1991  
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor submitted to the EMBL Data Library. May 1995  
A;Description: Characterization of the promoter region of the murine p75-TNF receptor  
A;Accession: A40254  
A;Reference number: S54816  
A;Accession: S54816  
A;Status: Preliminary  
A;Molecule type: DNA  
A;Residues: 1-22 <KIS>  
A;Cross-references: EMBL:X87128; NID:9809043; PIDN:CAA60618\_1; PID:9809044  
C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolog  
C:Keywords: cytokine receptor; transmembrane protein  
F;1-22/Domain: signal sequence #status predicted <SIG>  
F;23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>  
F;40-77/Domain: NGF receptor repeat homology <NG3>  
F;78-120/Domain: NGF receptor repeat homology <NG4>  
F;166-203/Domain: NGF receptor repeat homology <NG4>

Query Match 26.0%; Score 295; DB 2; Length 474; Best Local Similarity 34.0%; Pred. No. 3. 5e-15; Indels 20; Gaps 8; Matches 66; Conservative 24; Mismatches 84; Indels 20; Gaps 8;  
QY 8 PYASE NOTCQDQEKEYEPQRICRCSRCPTIVNSAKCSRIRDDTVCAENSYHN 66  
Db 31 PYKPERCYPECQISQ-EYDRAQMCKCPQGYVKHCKNITSDTVGADCEASMYTWN 89  
QY 67 YLTICQLCR--PDCPVNGLEETAPCTSKRKTIQCRCQGMFCA-AWAECTHCELLSDC 121

Db 90 QFRTCLSSSSCQTDQV---ELRACRQNRVCAGRYCALKTHSGSCQQCMWLSKC 145  
 Qy 122 PPGTEAELKDEDEVKGNNHCPKAGHPTSSPARGHPTCENGIVLEAAPGTAQSDT 181  
 Db 146 GGF-GVASSRAPNGVNICKACARGTISSTDTISDVORPHRTCS---ILATPGNASTDA 200  
 Qy 182 TCKNPFLPFPLPEMS 195  
 Db 201 VC---AFESPTLS 210

## RESULT 4

148854 gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 27-Oct-2003  
 C;Accession: J48854  
 R;Powell, E.E.; Wicker, L.S.; Peterson, I.B.; Todd, J.A.  
 Mamm. Genome 5, 726-727, 1994  
 A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.  
 A;Reference number: 148854; MUID:95178848; PMID:7873884  
 A;Accession: 148854  
 A;Status: preliminary; translated from GB/EMBL/DDJB  
 A;Molecule type: mRNA  
 A;Residues: 1-459 <RES>  
 A;Cross-references: EMBL:X76401; NID:9433830; PIDN:CA453981.1; PID:9433831  
 C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolog F;151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 25.6%; Score 290; DB 2; Length 459;  
 Best Local Similarity 33.5%; Pred. No. 8.2e-15; Mismatches 85; Indels 20; Gaps 8;  
 Matches 65; Conservative 24; Mismatches 85; Indels 20; Gaps 8;

Qy 8 PYASE-NOTCDQEKEYYEPORHICCSRCPGTYVSAKCSRIRDVCATCAENSNEHN 66  
 Db 16 PYKPERGYECQISO-EYDRAKAQMCARCPGQYVRFNCNKTSDTCADCEASMYTQWN 74  
 Qy 67 YLTICOLCR---PCDPVMPFEEIACTTSRKTKCQCPQSMFCA---AWALECTHECELLSOC 121  
 Db 75 QFRTCIUSCSSCSTDQV---ETRACTKDKOVRVACEARYCALKTHSOSCRQMLSKC 130  
 Qy 122 PRGEAEELKDEEVKGNNHCPKAGHPTSSPARGHPTCENGIVLEAAPGTAQSDT 181  
 Db 131 GPGF-GVASSRAPNGVNICKACAGTFSITSSDVCRPHRTCS---ILATPGNASTDA 185  
 Qy 182 TCKNPFLPFPLPEMS 195  
 Db 185 VC---AFESPTLS 195

A;Experimental source: Burkitt lymphoma cell line Raji  
 C;Genetics:  
 A;Gene: GDI; CD40  
 A;Cross-references: GDB:215268; OMIM:109535  
 A;Map position: 20q12-20q13.2  
 C;Superfamily: CD27 antigen; NGF receptor repeat homology  
 C;Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein  
 F;1-20/Domain: signal sequence #status predicted <SIG>  
 F;21-277/Domain: B-cell activation protein CD40 #status experimental <MAT>  
 F;21-193/Domain: extracellular #status predicted <EXT>  
 F;194-215/Domain: transmembrane #status predicted <TMM>  
 F;216-277/Domain: intracellular #status predicted <CYT>  
 F;153,180/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 24.5%; Score 278; DB 2; Length 277;  
 Best Local Similarity 35.0%; Pred. No. 4.4e-14; Mismatches 83; Indels 12; Gaps 5;  
 Matches 62; Conservative 20; Mismatches 83; Indels 12; Gaps 5;

Qy 7 PPYASINQTCRDQERKEYYEPORHICCSRCPGTYVSAKCSRIRDVCATCAENSNEHN 66  
 Db 22 PPTA---GR---EYQYLNSQ---CCSLCPGQKQVSDCTEFERBCLPGESERLDWN 72  
 Qy 67 YLTICOLCRPCDPVMPGLEETAPCTSRRKTKCQCPQGMFCAWALFCATHCELLSDPPGTE 126  
 Db 73 RETHQHQHKYCDPNGLRVQOKGTSBTDTCTCEGWHCTSEA---CESCYLRHRSOSPFG 130  
 Qy 127 AEIJKEVGKANNHCPKAGHPTSSPARGHPTCENGIVLEAAPGTAQSDT 183  
 Db 131 VK-QPATGVSDTICECPCPVGFFPSNVSAFERKCHPWTSCETKDLVVOAGTNKTDV 186

## RESULT 6

A46476

B cell-associated surface molecule CD40, long splice form - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 17-Nov-2000

C;Accession: A46476; A46515  
 R;Torres, R.M.; Clark, E.A.  
 J; Immunol. 148, 620-626, 1992  
 A;Title: Differential increase of an alternatively polyadenylated mRNA species of murine CD40  
 A;Reference number: 92105763; PMID:11370315  
 A;Accession: A46476  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-305 <TOR>

A;Cross-references: GB:M83312; NID:91553058  
 A;Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBI:75207)  
 A;Note: this translation is not annotated in GenBank entry MUSCD40A, release 11.3.0  
 R;Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne, J.; Immunol. 149, 3921-3926, 1992  
 A;Title: Genomic structure and chromosomal mapping of the murine CD40 gene.  
 A;Reference number: A46515  
 A;Accession: A46515  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: nucleic acid  
 A;Residues: 1-287, IV<GR>  
 A;Cross-references: GB:M8312; NID:91553058; PIDN:AA080705.1; PID:91553059; GB:M94126;  
 A;Experimental source: BALB/c, liver  
 A;Not: sequence extracted from NCBI backbone (NCBIP:120357)  
 C;Comment: For an alternative splice form, see PIR:A46475.  
 C;Comment: For an alternative splice form, see PIR:A46515.  
 C;Superfamily: CD27 antigen; NGF receptor repeat homology  
 C;Keywords: alternative splicing; transmembrane protein  
 F;105-144/Domain: NGF receptor repeat homology <NGF>

## RESULT 5

146771 B-cell activation protein CD40 precursor - human  
 C;Species: Homo sapiens (man)  
 C;Accession: 03-Jun-1993 #sequence\_revision 03-Feb-1994 #text\_change 21-Jul-2000  
 R;Stamenkovic, I.; Clark, E.A.; Seed, B.  
 EMBJ. 8, 1403-1410, 1989  
 A;Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor  
 A;Reference number: S04460; MUID:89356608; PMID:2475341  
 A;Accession: S04460  
 A;Molecule type: mRNA  
 A;Residues: 1-277 <STA>  
 A;Cross-references: EMBL:X60592; NID:929850; PIDN:CAA43045.1; PID:929851  
 R;Bergs-Andersen, S.; Paulie, S.; Kho, H.; Aspenstrom, P.; Perlmann, P.  
 J. Immunol. 142, 562-567, 1989  
 A;Title: Biochemical characteristics and partial amino acid sequence of the receptor-like  
 A;Reference number: A60771; MUID:8903941; PMID:2463309  
 A;Molecule type: protein  
 A;Residues: 21-50 <BR>

Query Match 21.5%; Score 243.5; DB 2; Length 305;  
 Best Local Similarity 31.0%; Pred. No. 1.9e-11; Mismatches 81; Indels 17; Gaps 5;  
 Matches 54; Conservative 22; Mismatches 81; Indels 17; Gaps 5;

Qy 15 TCDQEKEYYEPORHICCSRCPGTYVSAKCSRIRDVCATCAENSNEHWYLTCOLC 74  
 Db 25 TSD---KOYLHQQ---CCDLCPGPGRSLSHCTALEKQHCDSDGEISAQMREIRHQH 80

Query Match 19.6%; Score 222.5; DB 2; Length 271;  
 Best Local Similarity 32.1%; Pred. No. 6.7e-10; Indels 5;  
 Matches 53; Conservative 17; Mismatches 68; Gaps 5;

Qy 75 RPPCDPVGMLEETAPCTSKRKTCRQCRGFMCAAWALECTHCELLSDCPG----TEAEL 129  
 Db 81 RHECPNQGLRVIKKEGRPRESDTCTCERGQHCT--SKDCEACQRHTPCIPGRCMUMET 138

Qy 130 KDEVKGKNNHCVCPCKAGHFQNNTSSPSARCSQPTTRCENQGLVEAAGTAQSDTIC 183  
 Db 139 TTVV-----CHPCPVGFNSNOSSLFRKCYPWTISCEDKNLEVLQKGRSQTNWIC 186

**RESULT 7**

JCT705  
 death receptor-5 - chicken  
 C;Species: Gallus gallus (chicken)  
 C;Date: 09-Nov-2001 #sequence\_change 09-Nov-2001 #text\_change 09-Nov-2001  
 C;Accession: JCT705  
 A;Residues: 1-651 <BRI>  
 A;Cross-references: GB:AF349908  
 C;Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs to the death receptor, a cell death and/or survival signaling cascade.  
 C;Genetics:  
 A;Gene: dr-6  
 C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
 C;Keywords: ovary  
 F;1-21/Domain: signal sequence #status predicted <SIG>  
 F;332-352/Domain: extracellular cysteine-rich, ligand-binding #status predicted <TM>  
 F;410-475/Domain: death domain #status predicted <DED>  
 F;551-651/Region: conserved cytoplasmic #status predicted

Query Match 20.0%; Score 226.5; DB 2; Length 651;  
 Best Local Similarity 28.8%; Pred. No. 6.5e-10;  
 Matches 49; Conservative 26; Mismatches 62; Indels 33; Gaps 6;

Qy 30 ICCSICCPGTVYSAKSRTIDTVCATCAEANSYNEHWNLITICOLCR-PCDPVMGLEIAP 88  
 Db 50 L1C1DKCPAGTVYVSKHCTKSTRRECSPCPDGTFTKHENGTFERCHPKPCE-LPMIEKTH 107

Qy 89 CTSKRKHQCRQGPQGMF----CAAAELECTHCELLSDCPG----PGTBRKELKOEVGKG 136  
 Db 108 CTALTDRECTCILSGTQINDPCKVTV-----CPVQWGVRKKGTE----- 149

Qy 137 NHHCVVCKASQHQTSPSACQPHRCENGLVLAAPGIAQSDTICKAP 186  
 Db 150 DVRCKPCLRGIFSDVSSVMCKTYDCFGKMWVVKPGTESDNVCXSP 199

**RESULT 8**

S12783  
 OX40 antigen precursor - rat  
 N;Alternate names: nerve growth factor receptor homolog  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 30-Sep-1993 #sequence\_change 30-Sep-1993 #text\_change 05-Nov-1993  
 C;Accession: S12783; S08036  
 A;Cross-references: EMBL:X8214; PID:CAA59476.1; PID:9732819  
 A;Gene: ox40  
 A;Cross-references: EMBL:Z21674; PID:CAA79772.1; PID:9312828  
 A;Status: translated from GB/EMBL/DDBJ  
 A;Residues: 1-14; G, 16-272 <RE2>  
 A;Reference number: 148334; MUID:95255413; PMID:7737295  
 A;Molecule type: DNA  
 A;Gene: ox40  
 A;Cross-references: EMBL:X8214; PID:9732818; PID:9732819  
 C;Genetics:  
 A;Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1  
 C;Superfamily: CD27 antigen; NGF receptor repeat homology  
 Query Match 18.9%; Score 214.5; DB 2; Length 272;  
 Best Local Similarity 31.7%; Pred. No. 2.7e-09;  
 Matches 53; Conservative 16; Mismatches 67; Indels 31; Gaps 6;

Qy 21 KEYPEFHRCCSRCPGTVYSAKSRTIDTVCATCAEANSYNEHWNLITICOLCRCPDPV 80  
 Db 29 KRTYPSCHK-CCRECOPGHGMNSRCDHTRDTCHECTGEFYNEAVMDT-CKQCTQCNR 86

Qy 81 MGLEEATPCTSKRKTCRQCRGFMCAAWALECTHCELLSDCPGTRAEKLEUVGKNNHC 140  
 Db 87 SGSELKONCTPQDVTYCR-----PGTQR-QDSGYKGVDC 123

Qy 141 VPCKASHQNTSSP--SARCQPHRCENQGLVEAAGTAQSDTIC 185  
 Db 124 VPCPPGHF---SPGNNDQACKPWNTCTLSKGOTRHPSASLDACED 166

**RESULT 9**

I48700  
 gene ox40 protein - mouse  
 N;Alternate names: OX40 antigen  
 C;Species: Mus musculus (house mouse)  
 C;Accession: 02-Jul-1996 #sequence\_change 02-Jul-1996 #text\_change 11-Jan-2000  
 R;Calderhead, D.M.; Bahlmann, J.E.; van den Bertwegh, A.J.; Claassen, E.; Noelle, R.J.; J. Immunol. 151, 5261-5271, 1993  
 A;Title: Cloning of mouse OX40, a T cell activation marker that may mediate T-B cell interaction  
 A;Reference number: I48700; MUID:94044750; PMID:8228223  
 A;Accession: I48700  
 A;Status: translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-272 <RES>  
 A;Cross-references: EMBL:Z21674; PID:9312828  
 A;Status: translated from GB/EMBL/DDBJ  
 A;Residues: 1-14; G, 16-272 <RE2>  
 A;Reference number: 148334; MUID:95255413; PMID:7737295  
 A;Molecule type: DNA  
 A;Gene: ox40  
 A;Cross-references: EMBL:X8214; PID:CAA59476.1; PID:9732819  
 C;Genetics:  
 A;Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1  
 C;Superfamily: CD27 antigen; NGF receptor repeat homology  
 Query Match 18.9%; Score 214.5; DB 2; Length 272;  
 Best Local Similarity 31.7%; Pred. No. 2.7e-09;  
 Matches 53; Conservative 16; Mismatches 67; Indels 31; Gaps 6;

Qy 21 KEYPEFHRCCSRCPGTVYSAKSRTIDTVCATCAEANSYNEHWNLITICOLCRCPDPV 80  
 Db 29 KRTYPSCHK-CCRECOPGHGMNSRCDHTRDTCHECTGEFYNEAVMDT-CKQCTQCNR 86

Qy 81 MGLEEATPCTSKRKTCRQCRGFMCAAWALECTHCELLSDCPGTRAEKLEUVGKNNHC 140  
 Db 87 SGSELKONCTPQDVTYCR-----PGTQR-QDSGYKGVDC 123

Qy 141 VPCKASHQNTSSP--SARCQPHRCENQGLVEAAGTAQSDTIC 185  
 Db 124 VPCPPGHF---SPGNNDQACKPWNTCTLSKGOTRHPSASLDACED 166

**RESULT 10**

G0UT1  
 tumor necrosis factor receptor 1 precursor [validated] - human  
 N;Alternate names: P55 tumor necrosis factor receptor, TNF receptor type 1  
 N;Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein  
 C;Species: Homo sapiens (man)  
 C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 08-Dec-2000  
 C;Accession: A38208; A34893; A34900; A36555; C36555; A39281; S12057; J70758; A60231; A720-271/Domain: transmembrane #status predicted <TM>  
 F;211-235/Domain: transmembrane #status predicted <TM>  
 R;Fuchs, P.; Strehl, S.; Dworzak, M.; Himmer, A.; Ambros, P.F.

Genomics 13, 219-224, 1992  
A;Title: Structure of the human TNF receptor 1 (p60) gene (TNFR1) and localization to ch  
A;Reference number: A38208; MUID:92250049; PMID:1315717  
A;Accession: A38208  
A;Molecule type: DNA  
A;Residues: 1-455 <FUG>  
A;Cross-references: GB:W75864; GB:W75865; GB:W75866; NID:933974B; PIDN:AA61201.1; PID:9  
R;Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gantz, R.; Brockhaus, M.; Tabuchi, H.; Lesslau  
Cell 61, 351-359, 1990  
A;Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor  
A;Reference number: A34899; MUID:90235284; PMID:2158862  
A;Accession: A34899  
A;Molecule type: mRNA  
A;Residues: 1-455 <IOE>  
A;Cross-references: GB:W58286; GB:M33480; NID:9339753; PIDN:AAA36753.1; PID:9339754  
A;Experimental source: placenta  
A;Note: part of this sequence, including the amino end of the mature protein, confirmed  
R;Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaea, T.  
Cell 61, 361-370, 1990  
A;Title: Molecular cloning and expression of a receptor for human tumor necrosis factor.  
A;Reference number: A34900; MUID:90235285; PMID:2158863  
A;Accession: A34900  
A;Molecule type: mRNA  
A;Residues: 1-455 <SCH>  
A;Cross-references: GB:M33294; NID:9339744; PIDN:AAA03210.1; PID:9339745  
R;Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.;  
DNA Cell Biol. 9, 705-715, 1990  
A;Title: Molecular cloning and expression of human and rat tumor necrosis factor receptor  
A;Reference number: A36555; MUID:9109841; PMID:1702293  
A;Accession: A36555  
A;Molecule type: mRNA  
A;Residues: 1-455 <HIM>  
A;Cross-references: GB:M63121; NID:9339755; PIDN:AAA36754.1; PID:9339756  
A;Accession: C36555  
A;Molecule type: protein  
A;Residues: 30-38;11-53,'X',55-79,'XX',82-94,'NK';'XX',100-104,107-128,162-167,'X',169-2  
A;Note: the purified protein, called tumor necrosis factor binding protein, is a soluble  
R;Gray, P.W.; Barrett, K.; Chantrey, D.; Turner, M.; Feldmann, M.  
Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990  
A;Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of re  
A;Reference number: A38281; MUID:91017509; PMID:2170974  
A;Accession: A38281  
A;Molecule type: mRNA  
A;Residues: 1-455 <GRA>  
A;Cross-references: GB:M37764  
A;Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372  
R;Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann  
EMBO J. 9, 3269-3278, 1990  
A;Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the typ  
A;Reference number: S12057; MUID:91006021; PMID:1698610  
A;Accession: S12057  
A;Molecule type: mRNA  
A;Residues: 1-455 <NOP>  
A;Cross-references: EMBL:X55313; NID:937223; PRIM:CA39021.1; PID:937224  
A;Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, w  
R;Jemper, O.; Wallach, D.  
Gene 134, 203-216, 1993  
A;Title: Cloning and partial characterization of the promoter for the human p55 tumor ne  
A;Reference number: JN758; MUID:94085779; PMID:8262279  
A;Accession: JN758  
A;Molecule type: DNA  
A;Residues: 1-13 <KEM>  
R;Seckinger, P.; Vey, B.; Turcatti, G.; Wingfield, P.; Dayer, J.M.  
Eur. J. Immunol. 20, 1167-1174, 1990  
A;Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequenc  
A;Reference number: A60231; MUID:90292116; PMID:2113477  
A;Accession: A60231  
A;Molecule type: protein  
A;Residues: 41-43,'X',45-53,'X',55-57 <SEC>  
R;Satanga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Le  
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990  
A;Title: Purification and characterization of an inhibitor (soluble tumor necrosis facto

tients.

A;Reference number: A38258; MUID:91062364; PMID:2174164

A;Accession: A38258

A;Molecule type: protein

A;Residues: 41-60 <CAT>

A;Experimental source: cancer patient serum

R;Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thyssell, H.; Grubb, A.; Adolf, G.

Bur. J. Haematol. 42, 270-275, 1989

A;Title: Isolation and characterization of a tumor necrosis factor binding protein fro

A;Reference number: A60594; MUID:89171156; PMID:2924890

A;Accession: A60594

A;Molecule type: protein

A;Residues: 41-43,'X',45-53,'V',55-57,'XK',60 <OJS>

A;Experimental source: renal failure patient urine

J. Biol. Chem. 265, 1531-1535, 1990

A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence

A;Reference number: A35010; MUID:90110215; PMID:2153136

A;Accession: A35010

A;Molecule type: protein

A;Residues: 41-45 <ENG>

A;Experimental source: normal urine

R;Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.

Biochem. Biotechnol. Biochem. 58, 2266-2268, 1994

A;Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified

A;Reference number: JC2404; MUID:95128033; PMID:7765720

A;Accession: JC2404

A;Molecule type: protein

A;Residues: 41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201 <KAU>

A;Experimental source: urine

C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) a

C;Genetics:

A;Gene: GDB:TMFRI

A;Cross-references: GDB:125913; OMIM:191190

A;Map Position: 12p13.2-12p13.2

A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1

C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

C;Keywords: duplication; glycoprotein; receptor; transmembrane protein

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-455/Domain: tumor necrosis factor receptor 1 #status predicted <MAT>

F;30-211/Domain: extracellular #status predicted <EXT>

F;41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status

F;84-126/Domain: NGF receptor repeat homology <NG1>

F;127-167/Domain: NGF receptor repeat homology <NG2>

F;68-196/Domain: NGF receptor repeat homology <NG4>

F;212-234/Domain: transmembrane #status predicted <MEM>

F;23-455/Domain: intracellular #status predicted <INT>

F;44-82/Domain: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status predicted <INT>

F;44-82/Domain: NGF receptor repeat homology <NG1>

F;127-167/Domain: NGF receptor repeat homology <NG2>

Query Match

Best Local Similarity 18.6%; Score 210.5; DB 1, Length 455;

Matches 61; Conservative 19; Mismatches 84; Indels 23; Gaps 9;

QY 18 DQEK-----EXYEPQR--ICCSRCPGTYVSAKC-SRIRDWATCAENSTNEHWY 67  
Db 36 DREKRDSDSVCPQGKYIHPQNSICPKTCKHGTYLYNDCEPGFGQDTCRECESGSFTASEH 95

QY 68 LTICQLCRCPDPGYGLEEAPCTSKRKQCRQCPGMFCRAWA--LBCTHCELLSDFCPG 124  
Db 96 LRHCSCSKRKEMGQVEISSCTWDRIVGCRKRNQRYHWSNFQCNCSL--CLNG 152

QY 125 TEAEFLDEKVGNHHCVPKAGHE--QNTSSPSARQCQPHTRCENQGL--VEAAPGTAOSD 180

Db 153 TVHLSCQEE-KQVWCT-CHAGFIRENECVCSNCALKCIPQIENVKTEDSG 189

QY 181 TTCKNPRL 187

Db 210 TTVLLPL 216

RESULT 11

T28623

hypothetical protein G2R - variola major virus

C;Species: variola major virus

C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 15-Sep-2003

C;Accession: T28623

R;Massung, R.F.; Esposito, J.J.; Lai, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin

Nature 366, 748-751, 1993

A;Title: Potential virulence determinants in terminal regions of variola smallpox virus

A;Reference number: 220488; MUID:94088747; PMID:8264798

A;Accession: T28623

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Residues: 1-348 <MAS>

A;Cross-references: EMBL:122579; NID:9623595; PIDN:AAA60933.1; PID:9439102

A;Experimental source: strain Bangladesh 1975

C;Supfamily: TNF-alpha receptor-II; NGF receptor repeat homology

Query Match 18.5%; Score 210; DB 2; Length 348;

Best Local Similarity 29.0%; Pred. No. 7.1e-09; Mismatches 80; Indels 10; Gaps 5;

Matches 45; Conservative 20; MisMatches 80; Indels 10; Gaps 5;

QY 8 PYASENQTCRDQEKEYYEPQRHICCSRCPGTYVSAKSRSRIRDTWCATCAENSYEHWN 67

Db 23 PYTPPNKGCKDTEYK---RHNLCLSCPGTYASRLCDSKINTQCTPGSGFTSRNNH 78

QY 68 LTTCOLCR-PCDPVMGLIELAPTSKRKTQCRQCPGMFC-AAWALECTHELLSDCPGT 125

Db 79 LPACISCNGRON--SNOVETRSCTNHNRICECSPGIVCYCLKGSSGCKACVSQTKC--GI 134

QY 126 BAELKDEVKGKANNHCVPKAGHFQNTSSPSARCOP 160

Db 135 GYGVSHTSVGDVICSPCGFTSYHTVSSADKCEP 169

RESULT 12

D36858

N;Gene: G4R protein - variola virus

C;Species: variola virus

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 15-Sep-2003

C;Accession: D36858; S32385; S35987

R;Blinov, V.M.; Blinov, A.A.; Gytorov, V.V.; Pozdryakov, S.G.; Chizhikov, V.E.; Frol

submitted to GenBank, November 1992

A;Reference number: A36859

A;Accession: D36858

A;Molecule type: DNA

A;Residues: 1-349 <BLI>

A;Experimental source: strain India-1967, ssp. major, isolate Ind3

R;Kolykhalov, A.A.; Blinov, V.M.; Gytorov, V.V.; Pozdryakov, S.G.; Chizhikov, V.E.; Frol

submitted to the EMBL Data Library, April 1992

A;Description: Nucleotide sequence analysis of the region of Variola virus Xhol F O H P

A;Reference number: S46868

A;Accession: S46868

A;Molecule type: DNA

A;Residues: 1-349 <KOL>

A;Cross-references: EMBL:X67117; NID:9516428; PIDN:CAA17540.1; PID:9516449

A;Experimental source: strain India-1967, isolate Ind3

R;Shchelkunov, S.N.; Blinov, V.M.; Sandatchkiev, L.S.

FBS Lett. 319, 80-83, 1993

A;Title: Genes of variola and vaccinia viruses necessary to overcome the host protective

A;Reference number: S32385; MUID:9320281; PMID:8384129

A;Accession: S32385

A;Molecule type: DNA

A;Residues: 31-168 <SHC>

A;Cross-references: EMBL:X69198

A;Experimental source: strain India-1967, ssp. major

C;Genetics:

A;Gene: G4R

C;Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology <NGF>

F;32-66/Domain: NGF receptor repeat homology <NGF>

F;68-109/Domain: NGF receptor repeat homology <NG2>

F;110-151/Domain: NGF receptor repeat homology <NG3>

Query Match 18.5%; Score 210; DB 2; Length 349;

Best Local Similarity 29.0%; Pred. No. 7.1e-09; Mismatches 80; Indels 10; Gaps 5;

Matches 45; Conservative 20; MisMatches 80; Indels 10; Gaps 5;

QY 8 PYASENQTCRDQEKEYYEPQRHICCSRCPGTYVSAKSRSRIRDTWCATCAENSYEHWN 67

Db 24 PYTPPNKGCKDTEYK---RHNLCLSCPGTYASRLCDSKINTQCTPGSGFTSRNNH 79

QY 68 LTTCOLCR-PCDPVMGLIELAPTSKRKTQCRQCPGMFC-AAWALECTHELLSDCPGT 125

Db 80 LPACISCNGRON--SNOVETRSCTNHNRICECSPGIVCYCLKGSSGCKACVSQTKC--GI 135

QY 126 BAELKDEVKGKANNHCVPKAGHFQNTSSPSARCOP 160

Db 136 GYGVSHTSVGDVICSPCGFTSYHTVSSADKCEP 170

RESULT 13

D72175

N;Gene: G2R protein - variola minor virus (strain Garcia-1966)

C;Species: variola minor virus

C;Date: 24-Nov-1999 #sequence\_revision 24-Nov-1999 #text\_change 15-Sep-2003

C;Accession: D72175

R;Shchelkunov, S.N.; Totmenin, A.V.; Gutovov, V.V.; Safronov, P.F.; Massung, R.F.; Lopat

submitted to GenBank, March 1998

A;Description: Analysis of the complete coding sequence of DNA of alastrim variola mino

A;Reference number: A72150

A;Accession: D72175

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-349 <SHC>

A;Experimental source: strain Garcia-1966

C;Genetics:

A;Gene: G2R

C;Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology

Query Match 18.3%; Score 207; DB 2; Length 349;

Best Local Similarity 29.0%; Pred. No. 1.2e-08; Mismatches 81; Indels 10; Gaps 5;

Matches 45; Conservative 19; MisMatches 81; Indels 10; Gaps 5;

QY 8 PYASENQTCRDQEKEYYEPQRHICCSRCPGTYVSAKSRSRIRDTWCATCAENSYEHWN 67

Db 24 PYTPPNKGCKDTEYK---RHNLCLSCPGTYASRLCDSKINTQCTPGSGFTSRNNH 79

QY 68 LTTCOLCR-PCDPVMGLIELAPTSKRKTQCRQCPGMFC-AAWALECTHELLSDCPGT 125

Db 80 LPACISCNGRON--SNOVETRSCTNHNRICECSPGIVCYCLKGSSGCKACVSQTKC--GI 135

QY 126 BAELKDEVKGKANNHCVPKAGHFQNTSSPSARCOP 160

Db 136 GYGVSHTSVGDVICSPCGFTSYHTVSSADKCEP 170

RESULT 14

JC4302

N;Gene: tumor necrosis factor receptor p55 precursor - pig

C;Species: Sus scrofa domesticus (domestic pig)

C;Date: 29-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change 23-Jul-1999

C;Accession: JC4302; PC4093

R;Suter, B.; Pauli, U.

Gene 163, 263-266, 1995

A;Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.

A;Reference number: JC4302; MUID:96011645; PMID:7590278

A;Accession: JC4302

A;Molecule type: mRNA

A;Residues: 1-461 <STT>

A;Cross-references: GB:U1994; NID:91141752; PIDN:AC48499.1; PID:91141753

A;Gene: G4R

C;Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology <NGF>

F;32-66/Domain: NGF receptor repeat homology <NGF>

F;68-109/Domain: NGF receptor repeat homology <NG2>

A;Experimental source: kidney cell line 15  
 C;Genetics:  
 C;Gene: tnf  
 C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
 C;Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor  
 F;1-29/Domain: signal sequence #status predicted <S1G>  
 F;30-461/Product: tumor necrosis factor receptor type 1; NGF receptor repeat homology #status predicted <MM>  
 F;44-194/Domain: extracellular cysteine rich #status predicted <MM>  
 F;44-82/Domain: NGF receptor repeat homology <NG1>  
 F;84-126/Domain: NGF receptor repeat homology <NGF>  
 F;211-231/Domain: transmembrane #status predicted <MM>  
 F;361-447/Domain: signal transduction #status predicted <MM>  
 F;54-145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted <S1T>  
 Query Match 18.2%; Score 206; DB 2; Length 461;  
 Best Local Similarity 29.4%; Pred. No. 1.8e-08; Mismatches 77; Indels 38; Gaps 9;  
 Matches 57; Conservative 22; Mismatches 77; Indels 38; Gaps 9;  
 Qy 18 DQEKR----EYERPHR-TCCSERCPGIVYSAKC-SRIRDTCATCAENSYEHWNY 67  
 Db 36 DREKRESLCPCQKYSHPQRNSICCTKCHKGTYLHNDCLGPGDLTDRCENGTFASENH 95  
 Qy 68 LTICOLCRCPDPVMGLEEPLACTSKRTQRCQPEMFCAAWA---LECHCELLSDCPFG 124  
 Db 96 LTQCLCSKLRKSEMSVETISPCTIVDRDVTVCGRKRNQYRKWSETLFQCLNCSL--CPNG 152  
 Qy 125 TE---AEILODEVGKGNHCVPKKAGHFQMTSSPSARCQHTRCENQGLVEAFCIAQ-- 178  
 Db 153 TVQLPCLEKQDIT-----CNCHSGFFLR---DKECYSCVNCEKNADCNLCPATSEAR 201  
 Qy 179 -----SDTICKNPL 187  
 Db 202 NDFQDTGTVLILPL 215

---

RESULT 15  
 I37552  
 OX40 homolog - human  
 C;Species: Homo sapiens (man)  
 C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 11-Jan-2000  
 C;Accession: I37552  
 R;Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Ponat, EUR, J. Immunol. 24, 67-683, 1994  
 A;Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment  
 A;Reference number: 137552; PMID:94170844; PMID:7510440  
 A;Accession: I37552  
 A>Status: preliminary; translated from GB/EMBL/DDJB  
 A;Molecule type: mRNA  
 A;Residues: 1-277 <RES>  
 A;Cross-references: EMBL:X75962; NID:9472957; PID:CA53576.1; PID:9472958  
 C;Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 17.7%; Score 201; DB 2; Length 277;  
 Best Local Similarity 28.3%; Pred. No 2.8e-08;  
 Matches 49; Conservative 21; Mismatches 73; Indels 30; Gaps 5;

Qy 26 PQRHICCSPPGTVYSAKCSRDTDVCTCAENSYEHWNYLTCOLCRCPDPVMGLER 85  
 Db 37 PSNDRCHECCRCRPGNGWVSRCSRSNTVCRPCGRGFYNDWVSSKB-CKPTCTWCMLRSSER 95  
 Qy 86 LARTSKRTRQCRQGPQGMCAAWALETCFLISDCPPTAEALKDEVGRGNHHCVPKA 145  
 Db 96 KQJQTATQDPTVCRKCRAG-----TQPLDSYKQCD-----CAPCPP 130  
 Qy 146 GHFONTSSPSARSQPHTRGENQGLIVEAAPGTAQSDTTC-KNPLEPLPFEMSG 196  
 Db 131 GHF-SPSDNOACKEWINTLASHRLQDASNSDAICEDRDPATQPQBTQ 181

Search completed: August 28, 2004, 01:50:17

Job time : 42 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

### OM protein - protein search, using sw model

Run on: August 28, 2004, 01:33:14 ; Search time 25 Seconds  
(without alignments)  
410.313 Million cell updates/sec

Title: US\_10\_003-211-1  
Perfect score: 1133  
Sequence: 1 SQPQAVPPYASENQTCRDQE.....QSDTICKNPLPPLPPEMSGT 197

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SwissProt\_42;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1133	100.0	435	TNR3_HUMAN
2	771	68.0	415	TNR3_MOUSE
3	305	26.9	461	TTRB_HUMAN
4	295	26.0	474	TTRB_MOUSE
5	285.5	25.2	300	TRE_HUMAN
6	283	25.0	625	TTRI_MOUSE
7	278	24.5	275	TNR5_HUMAN
8	277	24.4	616	TRI1_HUMAN
9	251.5	22.2	269	TNR5_BOVIN
10	243.5	22.1	289	TNR5_MOUSE
11	242.5	21.4	401	TILB_MOUSE
12	239.5	21.1	401	TILB_HUMAN
13	235.5	20.8	401	TILB_RAT
14	230.5	20.3	283	TR14_HUMAN
15	228.5	20.0	655	TR21_HUMAN
16	226.5	20.0	655	TR21_MOUSE
17	225	19.9	349	CRMB_CAMPS
18	222.5	19.6	271	TNR4_RAT
19	214.5	18.9	272	TNR4_MOUSE
20	210.5	18.6	455	TR1A_HUMAN
21	210	18.5	349	TR1A_VARV
22	18.3	351	CRMB_COWPK	
23	205	18.2	461	TR1A_PIG
24	203	17.9	323	TNR6_BOVIN
25	201	17.7	277	TNR4_HUMAN
26	201	17.7	454	TR1A_MOUSE
27	196	17.3	595	TNR8_HUMAN
28	195.5	17.3	595	TNR9_HUMAN
29	194	17.1	332	TNR6_PIG
30	16.7	325	TTR2_STVKA	
31	16.7	471	TR1A_BOVIN	
32	184.5	16.3	461	TR1A_RAT
33	183.5	16.2	326	VT2_MIXVAL

### ALIGNMENTS

RESULT	ID	TNR3_HUMAN	STANDARD	PRT;	435 AA.
1	P3641	homo sapien			
2	P50284	mus musculus			
3	P20333	homo sapien			
4	P25119	mus musculus			
5	P0507	homo sapien			
6	035505	mus musculus			
7	P25242	homo sapien			
8	Q9YQG6	homo sapien			
9	Q28203	bos taurus			
10	P27512	mus musculus			
11	P08712	mus musculus			
12	000300	homo sapien			
13	008720	rattus norvegicus			
14	Q92556	homo sapien			
15	Q75309	homo sapien			
16	Q06055	mus musculus			
17	Q8WVAF	camelpox virus			
18	P15725	rattus norvegicus			
19	P47741	mus musculus			
20	P19438	homo sapien			
21	P34015	variola virus			
22	Q77559	cowpox virus			
23	P50555	sus scrofa			
24	P51867	bos taurus			
25	P43489	homo sapien			
26	P25118	mus musculus			
27	P28008	homo sapien			
28	Q07011	homo sapien			
29	Q77336	sus scrofa			
30	P25243	sheep fibroblast			
31	O19331	bos taurus			
32	P29334	rattus norvegicus			
33	P29825	myxoma virus			

RESULT 1  
TNR3\_HUMAN  
ID TNR3\_HUMAN  
AC P36911;  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 3 precursor  
(Lymphotxin-beta Receptor) (Tumor necrosis factor receptor 2 related protein) (Tumor necrosis factor C receptor).  
DE LTBR OR TNFRSF3 OR TNFCR.  
GN Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=liver;  
RX MEDLINE=2325281; PubMed=8486360;

BAENS M., CHAFFANET M., CASSIMAN J.J., DEN BERGHE H., MARYNEN P.; "Construction and evaluation of a hncDNA library of human 12p transcribed sequences derived from a somatic cell hybrid.", Genomics 16:214-218(1993).

RESULT 1  
TNR3\_HUMAN  
ID TNR3\_HUMAN  
AC P36911;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DE Tumor necrosis factor receptor superfamily member 3 precursor  
(Lymphotxin-beta Receptor) (Tumor necrosis factor receptor 2 related protein) (Tumor necrosis factor C receptor).  
DE LTBR OR TNFRSF3 OR TNFCR.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=lung;  
RX MEDLINE=22389257; PubMed=1247932;  
RA STRAUSSBERG R.D., REINGOLD E.A., GROUSE L.H., DERGE J.G., ALTMANER R.D., COLLINS F.S., WAGNER L., SHAMMEN C.M., SCHULER G.D., ALTCHUL S.F., ZEEBERG B., BUETON K.H., SCHAFER C.F., BHAT N.K., HOPKINS R.F., JORDAN H., MOORE T., MAX S.I., WANG J., HSIEH F., DIATCHENKO L., MARUSINA K., FARMER A.A., RUBIN G.M., HONG L., STAPLETON M., SOARES M.B., BONADIO M.F., CABAVANT T.L., SCHEETZ T.E., BROWNSTEIN M.J.J., USDIN T.B., TOSHII-YUKI S., CARNICCI P., SCHNEIDER C., RAHA S.S., LOQUELLANO N.A.J., PETERS G.J., ABRAMSON R.D., MULLAHY S.J., BOSK S.A., MCEWAN P.J., MCKERNAN K.J., MALEK J.A., GUARATNE P.H., RICHARDS S., WORLEY K.C., HALE S., GARCIA A.M., GAY L.J., HULKY S.W., VILLALON D.K., MUÑIZ D.M., SODERGREN B.J., LIU X., GIBBS R.A., RAFFERTY J., HEITON E., KETTEMAN M., MADEN A., RODRIGUES S., SANCHEZ A., WHITTING M., MADDAN A., YOUNG A.C., SNECHENKO Y., BOUFFARD G.G., BLAKESLEY R.W., TOUCHMAN J.W., GREEN E.D., DICKSON M.C., RODRIGUEZ A.C., GRIMWOOD J., SCHMITZ J., MYERS R.M., BUTTERFIELD Y.S.N., KIZYWINSKI M.I.I., SKALSKA U., SMAILUS D.E., RAJ, MEDLINE=9422209; PubMed=8171323;

CROWE P.D., VAN ARSDALE T.L., WALTER B.N., WARE C.F., HESSION C., EHRENFELS B., BROWNING J.L., DIN W.S., GOODWIN R.G., SMITH C.A.; "A Lymphotxin-alpha/beta-specific receptor.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [3]  
RP FUNCTION;  
CHARACTERIZATION.

RX MEDLINE=99223511; PubMed=1020706;  
 RA Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.;  
 RT "the cytoplasmic domain of the lymphotoxin-beta receptor mediates cell  
 death in HeLa cells.";  
 RL J. Biol. Chem. 274:11868-11873(1999).  
 RN [15] FT DOMAIN 249 435 CYTOPLASMIC (POTENTIAL).  
 RP FUNCTION.  
 RX MEDLINE=20261554; PubMed=10799510;  
 RA Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A.,  
 RA Whitbeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;  
 RT "The lymphotoxin-beta receptor is necessary and sufficient for  
 RT LIGHT-mediated apoptosis of tumor cells.";  
 RL J. Biol. Chem. 275:14307-14315(2000).  
 RN [16] FT REPEAT 42 81 TNFR-CYS 1.  
 RP INTERACTION WITH TRAF3.  
 RX MEDLINE=96218943; PubMed=8663299;  
 RA Nakano H., Oshima H., Chung W., Williams Abbott L., Ware C.F.,  
 RA Yagita H., Okumura K.;  
 RT "TRAF5, an activator of NF-kappaB and putative signal transducer for  
 RT the lymphotoxin-beta receptor.";  
 RL J. Biol. Chem. 271:14661-14664(1996).  
 RN [17] FT REPEAT 82 124 TNFR-CYS 2.  
 RP INTERACTION WITH TRAF4.  
 RX MEDLINE=98229299; PubMed=9626059;  
 RA Krajewski S., Zapata J.M., VanArsdale T.,  
 RA Gascogne R.D., Bebern K., McFadden D., Shabalk A., Hugh J.,  
 RA Reynolds A., Clevenger C.V., Reed J.C.,  
 RT "TRAF-4 expression in epithelial progenitor cells. Analysis in normal  
 RT adult, fetal, and tumor tissues.";  
 RL Am. J. Pathol. 152:1549-1561(1998).  
 RN [8] FT REPEAT 125 168 TNFR-CYS 3.  
 RP INTERACTION WITH TRAF5.  
 RX MEDLINE=9817245; PubMed=9511754;  
 RA Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,  
 RA Otsuka M., Yamamoto T., Inoue J.-I.;  
 RT "Cloning and characterization of a cDNA encoding the human homolog of  
 RT tumor necrosis factor receptor-associated factor 5 (TRAF5)." ;  
 RL Gene 207:135-140(1998).  
 CC LTA and LTB, and for TNFS14/LIGHT.  
 CC promotes apoptosis via TRAF3  
 and TRAF5. May play a role in the development of lymphoid organs.  
 CC --!- SUBFUNCTION: Receptor for the heterotrimeric lymphotoxin containing  
 CC and TRAF5. May play a role in the development of lymphoid organs.  
 CC --!- SUBFUNCTION: Associates with TRAF3, TRAF4 and TRAF5.  
 CC --!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC --!- SIMILARITY: Contains 4 TNFR-Cys repeats.

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RESULT 2  
 TNR3\_MOUSE STANDARD; PRT; 415 AA.  
 ID TNR3\_MOUSE  
 AC P50284;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 3 precursor  
 DE (Lymphotoxin-beta receptor).  
 DE TNFRSF3 OR TNFCR.  
 GN LTBR OR TNFRSF3 OR TNFCR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1] FT DOMAIN 249 435 CYTOPLASMIC (POTENTIAL).  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CVB; TISSUE=Lung;  
 RX MEDLINE=8607204; PubMed=7594541;  
 RA Force W.N., Walter B.N., Hession C., Tizard R., Kozak C.A.,  
 RA Browning J.L., Ware C.F.,  
 RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,  
 RT and expression." /J. Immunol. 155:5280-5288(1995).  
 RN [2] FT REPEAT 83 98 TNFR-CYS 4.  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96163805; PubMed=8586432;  
 RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,  
 RA Honjo T.;  
 RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal  
 RT sequence trap and chromosomal mapping." /J. Genomics 30:312-319(1995).  
 RL [3] FT DOMAIN 31 435 SUPERFAMILY MEMBER 3.  
 RP EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 31 227 POTENTIAL.

INTERACTION WITH TRAF5.

RC	STRAIN-BAL/B/C;	Db	148	VICOPGSTEAEVDEIMTDVNGCVPCKPGHONTSSPRARCPHTRCIEQGLVAAAGTSY
RX	MEDLINE=9628943; PubMed=8663299;	QY	179	SDTICKNPLEP 189
RA	Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,	CC	180	SDTICKNPPPEP 218
RA	Yagita H., Okumura K.;	CC	181	SDTICKNPPPEP 218
RT	"TRAF5, an activator of NF-kappaB and putative signal transducer for the lymphotoxin-beta receptor.";	CC	182	SDTICKNPPPEP 218
RT	J. Biol. Chem. 271:4661-4664 (1996).	CC	183	SDTICKNPPPEP 218
RL	-- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing LTA and LTB, and for TNFSF1/LIGHr. Promotes apoptosis via TRAF3 and TRAF5. May play a role in the development of lymphoid organs (By similarity).	CC	184	SDTICKNPPPEP 218
CC	-- SUBUNIT: Self-associates (By similarity). Associates with TRAF5.	CC	185	SDTICKNPPPEP 218
CC	-- ASSOCIATES WITH TRAF3 AND TRAF4 (By similarity).	CC	186	SDTICKNPPPEP 218
CC	-- SUBCELLULAR LOCATION: Type I membrane protein.	CC	187	SDTICKNPPPEP 218
CC	-- SIMILARITY: Contains 4 TNFR-Cys repeats.	CC	188	SDTICKNPPPEP 218
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DR	EMBL: U29173; AAA68964.1; --.	DR	190	SDTICKNPPPEP 218
DR	EMBL: L38423; AAB00546.1; --.	DR	191	SDTICKNPPPEP 218
DR	EMBL: U30798; AAAB81334.1; --.	DR	192	SDTICKNPPPEP 218
DR	HSSP: 014763; IDOG.	DR	193	SDTICKNPPPEP 218
DR	MGD: MGI:104875; Ltrb.	DR	194	SDTICKNPPPEP 218
DR	InterPro: IPR001368; TNFR_c6.	DR	195	SDTICKNPPPEP 218
Pfam: PF00020; TNFR_c6; 3.	PFAM: PF00020; TNFR_c6; 3.	DR	196	SDTICKNPPPEP 218
SMART: SM00208; TNFR_NeFr_1; 2.	SMART: SM00208; TNFR_NeFr_2; 3.	DR	197	SDTICKNPPPEP 218
PROSITE: PS00550; TNFR_NeFr_2; 3.	PROSITE: PS00550; TNFR_NeFr_2; 3.	DR	198	SDTICKNPPPEP 218
Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.	Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.	DR	199	SDTICKNPPPEP 218
SIGNAL	SIGNAL	DR	200	SDTICKNPPPEP 218
FT	CHAIN	FT	201	SDTICKNPPPEP 218
FT	31	FT	202	SDTICKNPPPEP 218
FT	415	FT	203	SDTICKNPPPEP 218
FT	DOMAIN	FT	204	SDTICKNPPPEP 218
FT	231	FT	205	SDTICKNPPPEP 218
FT	TRANSMEM	FT	206	SDTICKNPPPEP 218
FT	224	FT	207	SDTICKNPPPEP 218
FT	415	FT	208	SDTICKNPPPEP 218
FT	DOMAIN	FT	209	SDTICKNPPPEP 218
FT	245	FT	210	SDTICKNPPPEP 218
FT	REPEAT	FT	211	SDTICKNPPPEP 218
FT	42	FT	212	SDTICKNPPPEP 218
FT	REPEAT	FT	213	SDTICKNPPPEP 218
FT	82	FT	214	SDTICKNPPPEP 218
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FT	125	FT	216	SDTICKNPPPEP 218
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FT	171	FT	218	SDTICKNPPPEP 218
FT	DISUFID	FT	219	SDTICKNPPPEP 218
FT	43	FT	220	SDTICKNPPPEP 218
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FT	59	FT	222	SDTICKNPPPEP 218
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FT	62	FT	224	SDTICKNPPPEP 218
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FT	104	FT	230	SDTICKNPPPEP 218
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FT	40	FT	418	SDTICKNPPPEP 218
FT	CARBONYD	FT	419	SDTICKNPPPEP 218
FT	40	FT	420	SDTICKNPPPEP 218
FT	C			

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [6]  
 RP SEQUENCE OF 37-461 FROM N.A.  
 RX MEDLINE=91370690; PubMed=1966549;  
 RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.-W., Gentz R.,  
 RA Brockhaus M., Lesslauer W.;  
 RT "Two human TNF receptors have similar extracellular, but distinct  
 RT intracellular, domain sequences";  
 RL Cytokine 2:231-237(1990).  
 RN [7]  
 RP SEQUENCE OF 116-461 FROM N.A., PARTIAL SEQUENCE, AND VARIANT ARG-196.  
 RX MEDLINE=90149572; PubMed=2166946;  
 RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,  
 RA Ringold G.M.;  
 RT "Complementary DNA cloning of a receptor for tumor necrosis factor  
 and demonstration of a shed form of the receptor.>";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).  
 RN [8]  
 RP SEQUENCE OF 154-183 FROM N.A., AND VARIANTS ARG-196 AND LYS-232.  
 RX MEDLINE=21069356; PubMed=11197692;  
 RA Tauchiya N., Komata T., Matsushita M., Ohashi J., Tokunaga K.;  
 RT "New single nucleotide polymorphisms in the coding region of human  
 TNFR2: association with systemic lupus erythematosus.>";  
 RL Genes Immun. 1:501-503(2000).  
 RN [9]  
 RP SEQUENCE OF 27-31.  
 RX MEDLINE=90110215; PubMed=2153136;  
 RA Engelmajer H., Novick D., Wallach D.,  
 RT "Two tumor necrosis factor-binding proteins purified from human  
 urine. Evidence for immunological cross-reactivity with cell surface  
 tumor necrosis factor receptors";  
 RL J. Biol. Chem. 265:1531-1536(1990).  
 RN [10]  
 RP SEQUENCE OF 23-40: 65-69; 136-141; 300-306 AND 346-362.  
 RX MEDLINE=91056048; PubMed=2173696;  
 RA Loeffscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,  
 RA Brockhaus M.;  
 RT "Purification and partial amino acid sequence analysis of two  
 distinct tumor necrosis factor receptors from HL60 cells.>";  
 RL J. Biol. Chem. 265:20131-20138(1990).  
 RN [11]  
 RP CHARACTERIZATION.  
 RX MEDLINE=301640; PubMed=1328224;  
 RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,  
 RA Lipari M.T., Goeddel D.V.;  
 RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.  
 Characterization of ligand binding, internalization, and receptor  
 phosphorylation.>";  
 RL J. Biol. Chem. 267:21172-21178(1992).  
 RN [12]  
 RP INTERACTION WITH TRAF2.  
 RX MEDLINE=94134937; PubMed=8069016;  
 RA Rothe M., Wong S.C., Henzel W.J., Goeddel D.V.;  
 RT "A novel family of putative signal transducers associated with the  
 cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.>";  
 RL Cell 78:681-692(1994).  
 RN [13]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH  
 TRAF2.  
 RX MEDLINE=94221490; PubMed=10206649;  
 RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;  
 RT "Structural basis for self-association and receptor recognition of  
 human TRAF2.>";  
 RL Nature 398:533-538(1999).  
 RN [14]  
 RP VARIANTS ARG-196 AND LYS-232.  
 RX MEDLINE=21603988; PubMed=11762942;  
 RA Morita C., Horiochi T., Tsukamoto H., Hatta N., Kikuchi Y.,  
 RA Arinobu Y., Otsuka T., Sawabe T., Harashima S., Nagasawa K., Niho Y.;  
 RT "Association of tumor necrosis factor receptor type II polymorphism

RT 196R with systemic lupus erythematosus in the Japanese: molecular and  
 RT functional analysis";  
 RT Arthritis Rheum. 44:2819-2827(2001).  
 RL [15]  
 RP VARIANT ARG-196.  
 RX MEDLINE=22151311; PubMed=12161545;  
 RA Perai B., San Millan J.L., Castello R., Moghetti P.,  
 RA Escobar-Morreale H.F.;  
 RT "Comment: the methionine 196 arginine polymorphism in exon 6 of the  
 TNF receptor 2 gene (TNFRSF1B) is associated with the polycystic  
 RT ovary syndrome and hyperandrogenism.>";  
 RL J. Clin. Endocrinol. Metab. 87:3977-3983(2002).  
 CC -!- FUNCTION: Receptor with high affinity for TNFRSF2/TNF-alpha and  
 CC approximately 5-fold lower affinity for homotrimeric  
 CC TNFRSF1/TNF2 complex recruits the TNFRSF1/TNF2 complex to TNFRSF1B/TNFR2. The TNF  
 CC receptor 2 mediates most of the metabolic effects of TNF-alpha.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein and secreted.  
 CC -!- PTM: Phosphorylated; mainly on serine residues and with a very low  
 CC level on threonine residues.  
 CC -!- PTM: A soluble form (tumor necrosis factor binding protein 2) is  
 CC produced from the membrane form by proteolytic processing.  
 CC -!- PHARMACEUTICAL: Available under the name Enbrel (Immunex and  
 CC Wyeth-Ayerst). Used to treat moderate to severe rheumatoid  
 CC arthritis (RA). Enbrel consist of the extracellular ligand-binding  
 CC portion of TNFR2 linked to an Immunoglobulin Fc chain. It binds to  
 CC TNF-alpha and blocks its interactions with receptors.  
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC -!- DATABASE: NAME=PROW; URL=CD guide CD20b entry;  
 CC WWW="HTTP://www.ncbi.nlm.nih.gov/prow/cd/ccl20b.htm".  
 CC ---  
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 CC or send an email to license@isb-sib.ch).  
 CC ---  
 DR EMBL; M2315; AAC59929.1; -.  
 DR EMBL; US2165; AAC50622.1; -.  
 DR EMBL; US2156; AAC50622.1; JOINED.  
 DR EMBL; US2157; AAC50622.1; JOINED.  
 DR EMBL; US2158; AAC50622.1; JOINED.  
 DR EMBL; US2159; AAC50622.1; JOINED.  
 DR EMBL; US2160; AAC50622.1; JOINED.  
 DR EMBL; US2161; AAC50622.1; JOINED.  
 DR EMBL; US2162; AAC50622.1; JOINED.  
 DR EMBL; US2163; AAC50622.1; JOINED.  
 DR EMBL; US2164; AAC50622.1; JOINED.  
 DR EMBL; US2165; AAC50622.1; JOINED.  
 DR EMBL; M5594; AAC36755.1; -.  
 DR EMBL; AY264804; AAC89076.1; -.  
 DR EMBL; AX42040; AAC898939.1; -.  
 DR EMBL; BC02977; AAC82977.1; -.  
 DR EMBL; S63368; AB19824.2; -.  
 DR EMBL; M35957; AAC6262.1; -.  
 DR EMBL; AB030950; BAA89053.1; -.  
 DR PIR; A35356; A35356.  
 DR PDB; 1CR9; 12-APR-99.  
 DR Genew; HGNC:11917; TNFRSF1B.  
 Query Match 26.9%; Score 305; DB 1; length 461;  
 Best Local Similarity 35.0%; Pred. No. 4.9e-19;  
 Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;

QY 5 AVPPVASE-NOTCRDQEKEYEPQRHICSRPPGTVSAKSRSRIRTCATCAENSYNE 63  
 Db 28 AFTPYAEPGSGCR-LREYYDQTAQKCCSKCSPGQAHAKVFCTKTSITVCDSCEDSITQ 85  
 QY 64 HMYNYLTICOLCR--PDDPMVMLEBLAPCTSRKTCRCQPMFCAMWLE-CTHCEULS 119

**RESULT 4**

TRIB\_MOUSE STANDARD; PRT; 474 AA.

ID TRIB\_MOUSE STANDARD; PRT; 474 AA.

AC F25179; F97893;

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor necrosis factor receptor 2) (TNFR-R2) (p75).

GN TNFRSF1B OR TNFR2 OR TNFR-2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus. NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

MEDLINE=91187085; PubMed=1849278;

RA Lewis M., Tarraglia L.A., Lee A., Bennett G.L., Rice G.C., Wong G.H., Chen E.Y., Goeddel D.V.,

RT "Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific." Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834 (1991).

RN [2]

RP SEQUENCE FROM N.A.

RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I., Copeland N.G., Jenkins N.A., Smith C.A.,

RT "Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor." J. Mol. Cell. Biol. 11:3020-3026 (1991).

RN [3]

RP SEQUENCE OF 1-26 FROM N.A.

RC STRAIN=NOD;

RA Jacob C.O., Liu J., Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE OF 1-22 FROM N.A.

RC TISSUE=Liver;

RA Kissaneagh M., Fellowes R., Feldmann M., Chernajovsky Y., Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.

CC -- FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha and approximately 5-fold lower affinity for homotrimeric TNFR1/Lyphoxin-alpha. The TRAF1/TRAF2 complex recruits the apoptotic suppressors BIRC2 and BIRC3 to TNRSF1B/TNFR2 (By similarity).

CC --!- SUBUNIT: Binds to TRAF2 (By similarity).

CC --!- SUBCELLULAR LOCATION: Type I membrane protein.

CC --!- SIMILARITY: Contains 4 TNFR-Cys repeats.

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DR EMBL; M60469; AAH39752.1; -.

DR EMBL; M59378; AAQ40463.1; -.

DR EMBL; U39488; AAAB85021.1; -.

**RESULT 5**

TRIB\_HUMAN STANDARD; PRT; 300 AA.

ID TRIB\_HUMAN

AC 095407;

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DE 10-OCT-2003 (Rel. 42, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 6B precursor (Decoy receptor for Fas ligand) (Decoy receptor 3) (DccR3) (M6B).

DE GO:0007166; P:cell surface receptor linked signal transdu. . . ; IMP. GO:0008220; :necrosis; IMP. InterPro; IPR00136B; TNFR\_C6.

DR SMART; SW00208; TNFR\_4.

DR PROSITE; PS50052; TNFR\_NGFR\_1; 2.

DR PROSITE; PS50050; TNFR\_NGFR\_2; 3.

DR Receptor; Transmembrane; Glycoprotein; Repeat; Signal.

FT SIGNAL 1 22

FT CHAIN 23 474

FT DOMAIN 23 258

FT TRANSMEM 259 288

FT DOMAIN 289 474

FT REPEAT 77 119

FT REPEAT 78 119

FT REPEAT 120 164

FT REPEAT 165 203

FT DISULFID 40 54

FT DISULFID 55 68

FT DISULFID 58 76

FT DISULFID 79 94

FT DISULFID 97 111

FT DISULFID 101 119

FT DISULFID 121 127

FT DISULFID 136 145

FT DISULFID 139 163

FT DISULFID 166 181

FT CARBOHYD 169 69

FT CARBOHYD 195 195

FT CARBOHYD 195 195

FT SEQUENCE 474 AA; 50.1% MW: 462483.984746563 CRC64;

Query Match 26.0%; Score 295; DB 1; Length 474;

Best Local Similarity 34.0%; Pred. No. 3..6e-18;

Matches 66; Conservative 24; Mismatches 84; Indels 20; Gaps 8;

Db 31 PYKFBPGYEQIQISO-EYIDRKAQMCACKPPGQVKKHFQNKTSDIVCADCEASNYTQWN 89

QY 67 YLTICQQLCR---PDPVMGLEETAPCTSRSRKTKTQCQCPMFCA---AWALECTHCELLSNC 121

Db 90 QFRTCIQLSCSSSCTRTQV---ETRACTQOONQRYCAGRYCALKTHGSCRCQMLSK 145

QY 122 PPGETAELKDEVKGKNNHCVPCKAGHRQNTSSPARCOPHTRCENQGLVEAAGTAQSDT 181

Db 146 GPGF-GVASSRAPIGNVNLCKACAPGTFSDTTSIVCPHRICS---ILAIPGNSIDA 200

QY 182 TCKNPLEPLPEMS 195

Db 201 VC---APSPSPLS 210



RN	[1]
SEQUENCE FROM N.A.	
RC	RECEPTOR; Transmembrane; Glycoprotein; Repeat; Signal.
RC	TISSUE=Fetal liver;
RX	MEDLINE=9803277; PubMed=9367155;
RA	Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C., Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D., Galibert L.; "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function"; Nature 390:175-179 (1997).
RA	[21]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Thymus gland;
RX	MEDLINE=22389257; PubMed=12477932;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Ait-schul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Logueillo N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnarsson P.H., Richards S., Wollney K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Inn X., Gibbs R.A., Fahy J., Heitman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E., RA Scherneck A., Schein J.E., Jones S.J.M., Matra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RA	[3]
RP	FUNCTION:
RX	MEDLINE=99097247; PubMed=98787548;
CC	RA Nakagawa N., Kinosaki M., Yamaguchi K., Shima N., Yasuda H., Yano K., Morinaga T., Higashio K., "RANK is the essential signaling receptor for osteoclast differentiation factor in osteoclastogenesis"; Biochem. Biophys. Res. Commun. 253:395-400 (1998).
CC	RT - FUNCTION: Receptor for TNFSF11/RANKL/TRANCE/OPGL; essential for RANK-mediated osteoclastogenesis. Involved in the regulation of interactions between T-cells and dendritic cells.
CC	RT - SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF6 (By similarity).
CC	RT - SUBCELLULAR LOCATION: Type I membrane protein (potential).
CC	- - TISSUE SPECIFICITY: Ubiquitous expression with high levels in TRABECULAR BONE, THYMUS, SMALL INTESTINE, LUNG, BRAIN AND KIDNEY.
CC	- - WEAKLY EXPRESSED IN SPLEEN AND BONE MARROW.
CC	- - SIMILARITY: Contains 4 TNFR-Cys repeats.
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CC	-----
RESULT 7	
TNRS	HUMAN
ID	-TNR5_HUMAN STANDARD;
AC	P25942; Q9BYU0;
DT	01-MAY-1992 (Rel. 22, Last sequence update)
DT	15-MAR-2004 (Rel. 43, Last annotation update)
DE	Tumor necrosis factor receptor superfamily member 5 precursor (CD40L receptor) (B-cell surface antigen CD40) (CDw40) (BP50).
GN	TNFSF5 OR CD40.
OS	Homo sapiens (Human).
OC	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A. (ISOFORM 1):
RX	MEDLINE=8935608; PubMed=2475341;
RA	Stamenkovic I., Clark E.A., Seed B.; "A B-lymphocyte activation molecule related to the nerve growth factor receptor and induced by cytokines in carcinomas"; J. Biol. Chem. 268:1403-1410 (1989).
RA	[2]
RP	SEQUENCE FROM N.A. (ISOFORM 1):
RX	MEDLINE=21638749; PubMed=1780052;
RA	Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., Pfam; FF00020; TNFR_C6; 3.
RT	HSSP; P25942; 1C0F.
DR	MCD; MGI:1314891; TNfrsf5f.
DR	GO; GO:0007275; P: development; IMP.
DR	GO; GO:0007515; P: lymph gland development; IMP.
DR	EMBL; AF019046; AAC86910.1; -.
DR	EMBL; BC019185; AAH19185.1; -.
DR	DR
DR	HSSP; P25942; 1C0F.
DR	MCD; MGI:1314891; TNfrsf5f.
DR	GO; GO:0007275; P: development; IMP.
DR	GO; GO:0007515; P: lymph gland development; IMP.
DR	GO; GO:0001503; P: ossification; IMP.
DR	InterPro; IPR01368; TNFR_C6.
DR	Pfam; FF00020; TNFR_C6; 3.
DR	SMART; SM00208; TNFR_4.
DR	PROSITE; PS00652; TNFR_NGR_1; 1.
DR	PROSITE; PS50050; TNFR_NGR_2; 1.

- RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Cleee C.M.,  
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,  
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
RA Huckle B., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
RA Key M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
RA Lehvaeslahti M.H., Levershasha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
RA Marsh V.L., Martin S.L., McConnahe S.J., McLay K., McMurray A.,  
RA Milne S.A., Mistriy D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
RA Phillipine B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H.,  
RA Rice C.M., Ross M.T., Scott C.E., Seira H.K., Showkeen R., Sims S.,  
RA Skuce C.D., Smith M.L., Soderlund C.A., Steward J.E., Sulston J.E.,  
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Willis J.A.,  
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
RA Rogers J.;  
RT "The DNA sequence and comparative analysis of human chromosome 20.,";  
RL Nature 414:865-871(2001).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM II).  
RC TISSUE=Ovary;  
RX MEDLINE=2117110; PubMed=1172023;  
RA Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;  
RT "Regulation of CD40 function by its isoforms generated through  
RT alternative splicing";  
Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756 (2001).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM I).  
RC TISSUE=Ovary;  
RX MEDLINE=2238857; PubMed=12477932;  
RA Klausner R.D., Collins F.S., Grouse L.H., Derge J.G.,  
RA Strausberg R.L., Feingold E.R., Grouse L.H., Schaefer G.D.,  
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E.,  
RA Stapleton M., Soares M.B., Bandal M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uridin T.B., Yoshihiko T., Carnincip P., Prange C.,  
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McElwain R.J., Malek J.A., Gunnarson P.H.,  
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,  
RA Villalon D.K., Muzyk D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko G., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,  
RA Rodriguez A.C., Grinwood J.J., Schmutz J., Myers R.M., Smailus D.B.,  
RA Rodriguez Y.S.N., Skalska U., Skalska M.I.,  
RA Schneich A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [5]  
RP INTERACTION WITH TRAF3.  
RX MEDLINE=95129692; PubMed=753327;  
RA Cheng G., Cleary A.M., Ye Z.S., Hong D.T., Lederman S., Baltimore D.;  
RT "Involvement of Craf1, a relative of TRAF, in CD40 signaling.,";  
Science 267:1444-1448(1995).  
RN [6]  
RP INTERACTION WITH TRAF3.  
RX MEDLINE=95129692; PubMed=753326;  
RA Sato T., Irie S., Reed J.C.,  
RT "A novel member of the TRAF family of putative signal transducing  
RT proteins binds to the cytosolic domain of CD40.,";  
FEBS Lett. 358:113-118(1995).  
RN [7]  
RP INTERACTION WITH TRAF1; TRAF2; TRAF3 AND TRAF5.  
RX MEDLINE=98384149; PubMed=971306;  
RA Pullen S.S., Miller H.G., Everdeen D.S., Dang T.T., Crute J.J.,  
RA Kehry M.R.;  
RT "CD40-tumor necrosis factor receptor-associated factor (TRAF) interactions: regulation of CD40 signaling through multiple TRAF
- RT binding sites and TRAF hetero-oligomerization.,";  
RL Biochemistry 37:11836-11845(1998).  
RN [8]  
RP INTERACTION WITH TRAF5.  
RX MEDLINE=98172745; PubMed=9511754;  
RA Mizushima S.-I., Fujita M., Isida T., Azuma S., Kato K., Hirai M.,  
RA Otsuka M., Yamamoto T., Inoue J.-I.;  
RT "Cloning and characterization of a cDNA encoding the human homolog of tumor necrosis factor receptor-associated factor 5 (TRAF5).";  
RT Gene 207:135-140(1998).  
RN [9]  
RP INTERACTION WITH TRAF6.  
RX MEDLINE=98055703; PubMed=9432981;  
RA Kashiwada M., Shirakata Y., Inoue J.-I., Nakano H., Okazaki K.,  
RA Okumura K., Yamamoto T., Nagaoka H., Takemori T.,  
RT "Tumor necrosis factor receptor-associated factor 6 (TRAF6) stimulates extracellular signal-regulated kinase (ERK) activity in CD40 signaling along a ras-independent pathway.,";  
J. Exp. Med. 187:237-244 (1998).  
RN [10]  
RP 3D-STRUCTURE MODELING OF 24-144;  
RX MEDLINE=97189482; PubMed=9037712;  
RA Bajorath J., Aruffo A.;  
RT "Construction and analysis of a detailed three-dimensional model of the ligand binding domain of the human B cell receptor CD40.,";  
RL Proteins 27:59-70(1997).  
RN [11]  
RP 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.  
RX MEDLINE=98266353; PubMed=9605317;  
RA Singh J., Garber E., van Viljhmen H., Karpusas M., Hsu Y.-M.,  
RA Zheng Z., Naismith J.H., Thomas D.;  
RT "The role of polar interactions in the molecular recognition of CD40L with its receptor CD40.,";  
RL Protein Sci. 7:1124-1135(1998).  
RN [12]  
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF 247-266 IN COMPLEX WITH TRAF3.  
RX MEDLINE=20442386; PubMed=10984535;  
RA Ni C.Z., Welsh K., Leo E., Chiou C.K., Wu H., Reed J.C., ELY K.R.;  
RT "Molecular basis for CD40 signaling mediated by TRAF3.,";  
Proc. Natl. Acad. Sci. U.S.A. 97:10395-10399(2000).  
RN [13]  
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 178-195 IN COMPLEX WITH TRAF3.  
RX MEDLINE=22000222; PubMed=12005438;  
RA Li C., Ni C.Z., Havert M.L., Cabearas E., He J., Kaiser D., Reed J.C.,  
RA Satterthwait A.C., Cheng G., ELY K.R.;  
RT "Downstream regulator TANK binds to the CD40 recognition site on TRAF3.,";  
Structur. 10:403-411 (2002).  
RN [14]  
RP VARIANT HIGM3 ARG-83.  
RX MEDLINE=21532985; PubMed=11675497;  
RA Ferraris S., Giliani S., Insalaco A., Al-Ghonaium A.R., Sorresina A.R.,  
RA Louberer M., Avanzini M.A., Marconi M., Badolato R., Ugazio A.G.,  
RA Levy Y., Catalani N., Durandy A., Bakhi A., Notarangelo L.D.,  
RA Plebani A.;  
RT "Mutations of CD40 gene cause an autosomal recessive form of immunodeficiency with hyper IgM.,";  
Proc. Natl. Acad. Sci. U.S.A. 98:12614-12619(2001).  
RN [15]  
RP -!- FUNCTION: Receptor for TNFSF5/CD40L.  
CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform I);  
CC -!- SECRETED (isoform II).  
CC -!- ALTERNATIVE PRODUCTS:  
CC -!- Event=Alternative splicing; Named isoforms=2;  
CC -!- Comment=Additional isoforms seem to exist;  
CC Name\_I;  
CC IsoID\_P25942-1; Sequence=Displayed;  
CC Name=II;  
CC IsoID\_P25942-2; Sequence=VSP\_006472, VSP\_006473;  
CC -!- TISSUE SPECIFICITY: B cells and in primary carcinomas.  
CC -!- DISEASE: Defects in TNFRSF5 are the cause of hyper-IgM.

CC immunodeficiency type 3 (HTGM3) [MIM:606843]. HGM3 is an  
 CC autosomal recessive disorder which includes an inability of B  
 CC cells to undergo isotope switching, one of the final  
 CC differentiation steps in the humoral immune system, an inability  
 CC to mount an antibody-specific immune response, and a lack of  
 CC geminal center formation.

-!- SIMILARITY: Contains 4 TNFR-CYS repeats.  
 CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD40 entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm".

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 or send an email to license@isb-sib.ch).

DR EMBL; X60592; GAA43045.1; --.  
 DR AL035662; CAC17670.1; --.  
 DR EMBL; AJ300189; CACC924.1; --.  
 DR EMBL; BC012419; AAH12419.1; --.  
 DR PIR; S04450; A00771.  
 DR PDB; 1CDF; 01-APR-97.  
 DR PDB; 1FL1; 18-OCT-00.  
 DR PDB; 1L0A; 08-FEB-00.  
 DR PDB; 1CZZ; 26-SEP-01.

Query Match 24.5%; Score 278; DB 1; length 277;  
 Best Local Similarity 35.0%; Pred. No. 6.1e-17; length 277;  
 Matches 62; Conservative 20; MisMatches 83; Indels 12; Gaps 5;

QY 7 PPYASENQTCRQDEKEYYEPQRHICCSRCRGTYVSAKCSRIRDWCACTAENSNEHNW 66  
 Db 2 RPTA----CR--EKOYLNSQ---GCSLCGPQKLVDSDTEECLOGESERLDTN 72

QY 67 YLTICOLCRCPDPMVHLTAAPTSKRSRQTCRQCGMFCAAWAELCTHBLISDCPPGTE 126  
 Db 73 RETHCHHQKYCDPMLGRLVRQKGTSIDTCTCERGWHTSEA---CESCVLHRSGSPGF-G 130

QY 127 AELKOEUVGKNNHCYPCPKASHRQNNTSSPASRCOPTRCENQGLVIAAAPGTAQSTTC 183  
 Db 131 VK-QIATGVSDDTICBFPVGFPSNVSSAFERKHPWTSCTKDLVVOQAGINKTDWVC 186

RESULT 8

TRIL\_HUMAN STANDARD; PRT; 616 AA.

ID TRIL\_HUMAN STANDARD; PRT; 616 AA.

AC Q3Y5Q6; 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, last sequence update)  
 DT 10-OCT-2003 (Rel. 42, last annotation update)

DE Tumor necrosis factor receptor superfamily member 11A precursor  
 DE Receptor activator of NF-κB (osteoclast differentiation factor  
 receptor) (CD40).  
 GN TNFRSF1A OR RANK.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;  
 OX NCBI\_TaxID=9606;  
 RN [1] SEQUENCE FROM N.A.  
 RP TISSUE-Dendritic cell;  
 RX MEDLINE=9802977; PubMed=9367155;  
 RA Anderson D.M., Maraskovsky B., Billingsley W.L., Dougall W.C.,  
 RA Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.P., Cosman D.,  
 RA Galibert L.;  
 RT "A homologue of the TNF receptor and its ligand enhance T-cell growth  
 and dendritic-cell function.;"  
 RL Nature 390:175-179(1997).  
 RN [2] FUNCTION.  
 RP MEDLINE=99097247; PubMed=9878549;

RN CHAIN 30 616 TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11A.

RA Nakagawa N., Kinoshita M., Yamaguchi K., Shima N., Yasuda H., Yano K.,  
 RA Morinaga T., Higashio K.;  
 RT "RANK is the essential signaling receptor for osteoclast differentiation factor in osteoclastogenesis";  
 RT Biochem. Biophys. Res. Commun. 253:395-400(1998).  
 RN [3] INTERACTION WITH TRAF1; TRAF2; TRAF3; TRAF5 AND TRAF6.  
 RP RX MEDLINE=98447691; PubMed=9774460;  
 RA Wong B.R., Josien R., Lee S.Y., Vologodskaya M., Steinman R.M.,  
 Choi Y.;  
 RT "The TRAF family of signal transducers mediates Nr-kappaB activation by the TRANCE receptor";  
 RT J. Biol. Chem. 273:28355-28359(1998).  
 RN [4] VARIANT FEO LEU-LEU-CYS ALA-LEU-LEU-21 INS, VARIANT PDB2  
 RP ALA-LEU-LEU-LEU-LEU-CYS-ALA-LEU-LEU-21 INS, AND VARIANT VAL-192.  
 RX MEDLINE=20082806; PubMed=10615125;  
 RA Hughes A.F., Ralston S.H., Marken J., Bell C., MacPherson H.,  
 RA Wallace R.G., van Hul W., Whyte M.P., Nakatsuwa K., Hovv L.,  
 RA Anderson D.M.;  
 RT "Mutations in TNFRSF1A affecting the signal peptide of RANK, cause familial expansile osteolysis";  
 RL Nat. Genet. 24:45-48(2000).  
 CC -!- FUNCTION: Receptor for TNFRSF1/RANKL/TRANCE/OPGL; essential for  
 CC RANKL-mediated osteoclastogenesis. Involved in the regulation of  
 CC interactions between T-cells and dendritic cells.  
 CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.  
 CC -!- TISSUE SPECIFICITY: Ubiquitous expression with high levels in  
 CC skeletal muscle, thymus, liver, colon, small intestine and adrenal  
 CC gland.  
 CC -!- DISEASE: Defects in TNFRSF1A are the cause of familial expansile  
 CC osteolysis (FEO) [MIM:174810]. FEO is a rare autosomal dominant  
 CC bone disorder characterized by focal areas of increased bone  
 CC remodelling. The osteolytic lesions develop usually in the long  
 CC bones during early adulthood. FEO is often associated with early  
 CC onset deafness and loss of dentition.  
 CC -!- DISEASE: Defects in TNFRSF1A also known as familial Paget disease of  
 CC bone. PDB2 is a bone remodelling disorder with clinical  
 CC similarities to FEO. Unlike FEO, however, affected individuals  
 CC have involvement of the axial skeleton with lesions in the spine,  
 CC pelvis and skull.  
 CC -!- SIMILARITY: Contains 4 TNFR-CYS repeats.

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 or send an email to license@isb-sib.ch).

DR EMBL; A018253; AAB86809.1; --.  
 DR HSP; P25942; 1CDF.  
 DR Genew; HGNC:11908; TNFRSF1A.  
 DR MIM; 603499; --.  
 DR MIM; 602080; --.  
 DR MIM; 174810; --.  
 DR GO; GO:0004872; P:receptor activity; TAS.  
 DR GO; GO:0007267; P:cell-cell signaling; TAS.  
 DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.  
 DR GO; GO:0007165; P:signal transduction; TAS.  
 DR InterPro; IPR013368; TNFR\_c6.  
 DR PRO0020; TNFR\_C6\_4.  
 DR SMART; SM00208; TNFR\_4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS0050; TNFR\_NGFR\_2; 1.  
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;  
 KW Disease mutation; Deafness.  
 FT SIGNAL 29 POTENTIAL.  
 FT CHAIN 30 616 TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11A.

FT	DOMAIN	310	212	EXTRACELLULAR (POTENTIAL).
TRANSMEM	213	233	POTENTIAL.	
TRANSMEM	234	616	CYTOSMIC (POTENTIAL).	
DOMAIN	34	68	CYTOSMIC.	
REPEAT	34	68	TNFR-CYS 1.	
REPEAT	71	112	TNFR-CYS 2.	
REPEAT	114	151	TNFR-CYS 3.	
REPEAT	154	194	TNFR-CYS 4.	
DISULFID	34	46	BY SIMILARITY.	
DISULFID	47	60	BY SIMILARITY.	
DISULFID	50	68	BY SIMILARITY.	
DISULFID	71	86	BY SIMILARITY.	
DISULFID	92	112	BY SIMILARITY.	
DISULFID	114	127	BY SIMILARITY.	
DISULFID	133	151	BY SIMILARITY.	
CARBONYD	105	174	N-LINKED (GLCNAC. . .) (POTENTIAL).	
CARBONYD	21	21	L-> IIAILLLCIL (in PDB2).	
VARIANT	21	21	L-> LIICALL (in FEO).	
VARIANT	21	21	/FTID=VAR_011517.	
VARIANT	192	192	A-> V.	
VARIANT	192	192	/FTID=VAR_011518.	
SEQUENCE	616 AA;	66033 MW;	E3DE9AT08196F81 CRC64;	
Query Match	24.4%	Score 277; DB 1; Length 616;		
Best Local Similarity	31.7%	Pred. No. 1. 6e-16; Indels 14; Gaps 4;		
Matches	60;	Conservative 28; Mismatches 87;		
QY	4	QAVPVYASENQTCRDRQEKEYVPOHRICCSRCPPGTYVSAKCSRIRDTCATCLENSTNE 63		
Db	29	QRAAPCTSE-----KHYEHDGR-CCNKCGPKGMSKCTRTSDSVCLPCGCCDEYLQ 78		
QY	64	HNNVLITTCOLCRCPDPVMGLEETAPCTSKRKTOCRQPMFCAAWALECTHCELLSDCPP 123		
Db	79	SNWEDKDCLLHKVCDTGKALVAVVAGNSITPRRCACTAGYH--WSQDCECCRNTTECAP 135		
QY	124	GTFABLKDEVGKGNNHCVCKAGHFRONTSSPSACQPHTRCENGQGLVRAAPGTAQSDTTC 183		
Db	136	GLGAQHQPLQLNK-DTVCVKCLAGYFSDFSSTDKCRPWTNCITFLICKRVEHHGTEKSDAVC 194		
QY	184	KNPFLPPLP 192		
Db	195	SSSIPARKP 203		
RESULT 9				
TNRS5_BOVIN		STANDARD; PRT; 269 AA.		
ID				
AC				
DT	01-NOV-1997	(Rel. 35, Created)		
DT	01-NOV-1997	(Rel. 35, Last sequence update)		
DT	10-OCT-2003	(Rel. 42, Last annotation update)		
DE		Tumor necrosis factor receptor superfamily member 5 precursor		
DR		(CD40L receptor) (B-cell surface antigen CD40) (Fragment).		
GN		TNRSF5 OR CD40.		
OS		Bos taurus (Bovine).		
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Decora; Bovidae.		
OC		Bovidae; Bovinae; Bos.		
NCBI_TaxID	9913;			
RX	[1]	SEQUENCE FROM N.A.		
RX		MEDLINE=9728152; PubMed=9135560;		
RX		Hirano A., Brown W.C., Bates D.M.:		
RT		"Cloning, expression and biological function of the bovine CD40 homologue: role in B-lymphocyte growth and differentiation in cattle.";		
RT		ImmunoLOGY 90:294-300(1997).		
RL		-!- FUNCTION: Receptor for TNFSF5/CD40L.		
CC		-!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By similarity).		
CC		-!- SIMILARITY: Contains 4 TNFR-Cys repeats.		
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation of the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce">http://www.isb-sib.ch/announce</a> or send an email to license@isb-sib.ch).		
CC		CC EMBL; U57745; AAC48710.1; -.		
CC		DR P25942; ICDF; HSPB.		
CC		DR InterPro; IPR008063; Fas receptor.		
CC		DR InterPro; IPR001368; TNFR_c6.		
CC		DR Pfam; PF00208; TNFR_C6; 4.		
CC		DR PRINTS; PRO1680; FAS RECEPTOR.		
CC		DR SMARTI; SMC0208; TNFR_NGFR; 4.		
CC		DR PROSITE; PS50050; TNFR_NGFR; 2; 1.		
CC		KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.		
FT		FT SIGNAL 1 19 POTENTIAL.		
FT		FT CHAIN 20 >269 TUMOR NECROSIS FACTOR RECEPTOR.		
FT		FT DOMAIN 20 193 SUPERFAMILY MEMBER 5.		
FT		FT TRANSMEM 194 >269 EXTRACELLULAR (POTENTIAL).		
FT		FT DOMAIN 216 >269 CYTOSMIC (POTENTIAL).		
FT		FT REPEAT 25 60 TNFR-CYS 1.		
FT		FT REPEAT 61 103 TNFR-CYS 2.		
FT		FT REPEAT 104 144 TNFR-CYS 3.		
FT		FT REPEAT 145 187 TNFR-CYS 4.		
FT		FT DISULFID 26 37 BY SIMILARITY.		
FT		FT DISULFID 38 51 BY SIMILARITY.		
FT		FT DISULFID 41 59 BY SIMILARITY.		
FT		FT DISULFID 62 77 BY SIMILARITY.		
FT		FT DISULFID 83 103 BY SIMILARITY.		
FT		FT DISULFID 105 119 BY SIMILARITY.		
FT		FT DISULFID 111 116 BY SIMILARITY.		
FT		FT DISULFID 125 143 BY SIMILARITY.		
FT		FT CARBONYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT		FT CARBONYD 180 180		
FT		FT NON_TER 269 269 N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT		FT SEQUENCE 269 AA; 29983 MW; 74693F30:95F387 CRC64;		
Query Match	22.2%	Score 251.5; DB 1; Length 269;		
Best Local Similarity	33.1%	Pred. No. 1. 1e-14; Indels 9; Gaps 4;		
Matches	55;	Conservative 21; Mismatches 81; Indels 9; Gaps 4;		
QY	20	EKEVYEPORICCSRCPPGTYVSAKCSRIRDTCATCLENSTNEHNNVLTICOLCRPCD 79		
Db	28	EKQY--PNSLCCDLCPPQOKLVNDCTEVSKTECOSCIGKFLSTWNREKVCHEHRYCNP 85		
QY	80	VMGRLERIPEACTSKRKTOCRQPMFCAAWALECTHCELLSDCPPTEAELKDEVGGK--N 137		
Db	86	NLGRLIQSEGTTINTDTCVVEGHCTST--CBSCTPHSLICLRGFGVK--QIATGLLD 140		
QY	138	NHCYVCPKACKHFRONTSSPSACQPHTRCENGQGLVRAAPGTAQSDTTC 183		
Db	141	TVCBPCLPQFSNVAFFKCHRWTSCERKGLVRAAPGTAQSDTTC 186		
RESULT 10				
TNRS5_MOUSE		STANDARD; PRT; 289 AA.		
ID				
AC				
DT	01-AUG-1992	(Rel. 23, Created)		
DT	01-OCT-1996	(Rel. 34, Last sequence update)		
DT	10-OCT-2003	(Rel. 42, Last annotation update)		
DE		Tumor necrosis factor receptor superfamily member 5 precursor		
DR		(CD40L receptor) (B-cell surface antigen CD40) (BP50) (CDW40).		
GN		TNFSF5 OR CD40.		
OS		Mus musculus (Mouse).		
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OC		NCBI_TaxID=10090;		

RN [1] SSEQUENCE FROM N.A. (ISOFORM I).  
 RP DR EMBL; M94127; AAA7404.1; JOINED.  
 RX DR EMBL; AJ401387; CAC29427.1; -.  
 RA DR EMBL; AJ401388; CAC29428.1; -.  
 RT DR EMBL; AJ401389; CAC29429.1; -.  
 RT DR EMBL; AJ401390; CAC29430.1; -.  
 RL DR PIR; A46476; A6476.  
 RN DR HSSP; P25942; ICDF.  
 RP DR MGDB; MGI:86336; Tnfrsf5.  
 RC DR Interpro; IPR008063; Fas receptor.  
 RX DR Interpro; IPR001368; TNFR\_c6.  
 RA DR Pfam; PF00020; TNFR\_C6; 4.  
 RA DR PRINTS; PRO1680; FASRECEPTOR.  
 RT DR SMART; SM00208; TNFR.  
 RL DR PROSITE; PS00652; TNFR\_NFNR\_1; 1.  
 RN DR PROSITE; PS00652; TNFR\_NFNR\_2; 4.  
 RP DR Receptor; Transmembrane; Glycoprotein; Repeat; Signal;  
 V) KW Alternative splicing.  
 RX FT SIGNAL 1 19 POTENTIAL.  
 RA FT CHAIN 20 289 TUMOR NECROSIS FACTOR RECEPTOR  
 RT FT DOMAIN 20 193 SUPERFAMILY MEMBER 5.  
 RT FT TRANSMEM 194 215 EXTRACELLULAR (POTENTIAL).  
 RA FT DOMAIN 216 289 POTENTIAL.  
 RT FT REPEAT 25 60 CYTOPLASMIC (POTENTIAL).  
 RA FT REPEAT 61 103 TNFR-CYS 2.  
 RT FT REPEAT 104 144 TNFR-CYS 3.  
 RL FT DISULFID 25 187 TNFR-CYS 4.  
 RN FT DISULFID 38 37 BY SIMILARITY.  
 RP FT DISULFID 41 51 BY SIMILARITY.  
 RX FT DISULFID 62 77 BY SIMILARITY.  
 RA FT DISULFID 83 103 BY SIMILARITY.  
 RT FT DISULFID 105 119 BY SIMILARITY.  
 RL FT DISULFID 111 116 BY SIMILARITY.  
 RN FT DISULFID 125 143 BY SIMILARITY.  
 RP FT DISULFID 153 153 BY SIMILARITY.  
 RX FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 RA FT VARSPlic 166 203 SCEDDNLEVLQKGMQSQTNVICIGLERSMRMALLIVIPYNG ->  
 Yamanoto T., Inoue J.-I.;  
 RT FT RPKPPDASPAGHSQRCDGHPHHHFRGVSLYQKGGOETKG  
 "TRA5", a novel tumor necrosis factor receptor-associated factor  
 family protein, mediates CD40 signaling.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:9437-9442(1996).  
 CC !- FUNCTION: Receptor for TNFSF5/CD40L.  
 CC !- SUBUNIT: Interacts with TRAF3 and TRAF5. Interacts with TRAF1,  
 CC -! SUBCELLULAR LOCATION: Type I membrane protein (isoforms I, III, IV  
 and VI); secreted (isoform II).  
 CC !- ALTERNATIVE PRODUCTS:  
 CC Name=I;  
 CC IsoId=P27512-1; Sequence=Displayed;  
 CC Name=II;  
 CC IsoId=P27512-2; Sequence=VSP\_006474, VSP\_006475;  
 CC Name=III;  
 CC IsoId=P27512-3; Sequence=VSP\_006477, VSP\_006478;  
 CC Name=IV;  
 CC IsoId=P27512-4; Sequence=VSP\_006479, VSP\_006480;  
 CC Name=V;  
 CC IsoId=P27512-5; Sequence=VSP\_006476;  
 CC !- SIMILARITY: Contains 4 TNFR\_Cys repeats.  
 CC  
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 DR DR EMBL; M94127; AAA7404.1; JOINED.  
 DR DR EMBL; AJ401387; CAC29427.1; -.  
 DR DR EMBL; AJ401388; CAC29428.1; -.  
 DR DR EMBL; AJ401389; CAC29429.1; -.  
 DR DR EMBL; AJ401390; CAC29430.1; -.  
 DR DR PIR; A46476; A6476.  
 DR DR HSSP; P25942; ICDF.  
 DR DR MGDB; MGI:86336; Tnfrsf5.  
 DR DR Interpro; IPR008063; Fas receptor.  
 DR DR Interpro; IPR001368; TNFR\_c6.  
 DR DR Pfam; PF00020; TNFR\_C6; 4.  
 DR DR PRINTS; PRO1680; FASRECEPTOR.  
 DR DR SMART; SM00208; TNFR.  
 DR DR PROSITE; PS00652; TNFR\_NFNR\_1; 1.  
 DR DR PROSITE; PS00652; TNFR\_NFNR\_2; 4.  
 DR DR Receptor; Transmembrane; Glycoprotein; Repeat; Signal;  
 DR DR SIGNAL 1 19 POTENTIAL.  
 DR DR CHAIN 20 289 TUMOR NECROSIS FACTOR RECEPTOR  
 DR DR DOMAIN 20 193 SUPERFAMILY MEMBER 5.  
 DR DR TRANSMEM 194 215 EXTRACELLULAR (POTENTIAL).  
 DR DR DOMAIN 216 289 POTENTIAL.  
 DR DR REPEAT 25 60 CYTOPLASMIC (POTENTIAL).  
 DR DR REPEAT 61 103 TNFR-CYS 2.  
 DR DR REPEAT 104 144 TNFR-CYS 3.  
 DR DR REPEAT 145 187 TNFR-CYS 4.  
 DR DR DISULFID 25 37 BY SIMILARITY.  
 DR DR DISULFID 38 51 BY SIMILARITY.  
 DR DR DISULFID 41 59 BY SIMILARITY.  
 DR DR DISULFID 62 77 BY SIMILARITY.  
 DR DR DISULFID 83 103 BY SIMILARITY.  
 DR DR DISULFID 105 119 BY SIMILARITY.  
 DR DR DISULFID 111 116 BY SIMILARITY.  
 DR DR DISULFID 125 143 BY SIMILARITY.  
 DR DR CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 DR DR VARSPlic 166 203 SCEDDNLEVLQKGMQSQTNVICIGLERSMRMALLIVIPYNG ->  
 DR DR RPKPPDASPAGHSQRCDGHPHHHFRGVSLYQKGGOETKG  
 DR DR (in isoform III).  
 DR DR /FTId=VSP\_006474.  
 DR DR Missing (in isoform II).  
 DR DR /FTId=VSP\_006475.  
 DR DR GLKSRMRAITVPIVPMGILITIFGVFLYIK -> E (in  
 DR DR isoform V).  
 DR DR /FTId=VSP\_006476.  
 DR DR KKVKVKPKNQNEMLPPAARR -> SECSEBEREGGFSPVPA  
 DR DR S (in isoform III).  
 DR DR Missing (in isoform IV).  
 DR DR /FTId=VSP\_006477.  
 DR DR Missing (in isoform III).  
 DR DR /FTId=VSP\_006478.  
 DR DR KVVKKP -> SGQTKG (in isoform IV).  
 DR DR /FTId=VSP\_006479.  
 DR DR Missing (in isoform IV).  
 DR DR /FTId=VSP\_006480.  
 DR DR SEQUENCE 289 AA; 32111 MW; C791CB6D2FEA574E CRC64;  
 DR DR Query Match 21.5%; Score 243.5; DB 1; Length 289;  
 DR DR Best Local Similarity 31.0%; Pred. No. 5.6e-14; Gaps 5;  
 DR DR Matches 54; Conservative 22; Mismatches 81; Indels 17;  
 DR DR QY 15 TCRQPEKEYEPORHICCSRCPGTYVAKCSRRIIRDVTCACTAENSYMEHWNLITLCQIC 74  
 DR DR 25 TCSD--KQYLHDGQ--CCDLQCPQRSLTSHTALEKTQCHPCDSGEFSQAQNBRICHQ 80  
 DR DR QY 75 RPCDPVMGLEELAARTSKRSRKTCQRCPSMFCAAWELECTCELLSDCPG---TEAEL 129  
 DR DR 81 RHCBPNOGLRVKKGEGTAGTSDTVCIKEGQHCT--SKDCEAACHTPCLPGFGYMEMATE 138  
 DR DR QY 130 KDEVKGKNNHCVPKAGHQNTSSPARQPHTRCENGIVNEAPGTAOSDTC 183  
 DR DR 139 TDVY----CHCPVGFSNQSSLEEKCPWTSCKDRNLEVLOQTSQTNVIC 186  
 DR DR EMBL; M94128; AAA37404.1; JOINED.  
 DR DR EMBL; M94126; AAA37404.1; -.  
 DR DR EMBL; M94129; AAA37404.1; JOINED.  
 DR DR EMBL; M94128; AAA37404.1; JOINED.



- RESULT 12  
**TITLE\_HUMAN** STANDARD; PRT; 401 AA.  
**ID** T11B\_HUMAN  
**AC** 000300; 060235; 09UHP4;  
**DT** 28-FEB-2003 (Rel. 41, Last sequence update)  
**DT** 10-OCT-2003 (Rel. 42, Last annotation update)  
**DR** Tumor necrosis factor receptor superfamily member 11B precursor  
**DE** (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).  
**GN** TNFRSF1B OR OPG OR OCIF  
**OS** Homo sapiens (Human)  
**OC** Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
**OX** Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
**RN** [1] NCBI-TaxID=9606;  
**RP** SEQUENCE FROM N.A.  
**RC** TISSUE=Kidney;  
**RX** MEDLINE=97262071; PubMed=9108485;  
**RA** Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,  
**RA** Luethey R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,  
**RA** Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,  
**RA** Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Patterson W.,  
**RA** Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,  
**RA** Suggs S., Boyle W.J.;  
**RT** "Osteoprotegerin: a novel secreted protein involved in the regulation  
**RT** of bone density.";  
**RL** Cell 89:309-319(1997).  
**RN** [2]  
**RP** SEQUENCE FROM N.A.  
**RC** TISSUE=Lung cancer;  
**RX** MEDLINE=9815033; PubMed=9492069;  
**RA** Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,  
**RA** Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,  
**RA** Tsuda E., Morinaga T., Higashio K.;  
**RT** "Identity of osteoclastogenesis inhibitory factor (OCIF) and  
**RT** osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits  
**RT** osteoclastogenesis in vitro";  
**RL** Endocrinology 139:1329-1337(1998).  
**RN** [3]  
**RP** SEQUENCE FROM N.A., AND VARIANT ASN-3.  
**RC** TISSUE=Placenta;  
**RX** MEDLINE=98351569; PubMed=9688283;  
**RA** Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;  
**RT** "Cloning and characterization of the gene encoding human  
**RT** osteoprotegerin and charaterization of the gene encoding human  
**RL** Bur. J. Biochem. 254:685-691(1998).  
**RN** [4]  
**RP** SEQUENCE FROM N.A., AND VARIANT ASN-3.  
**RC** TISSUE=Eye;  
**RX** MEDLINE=22388257; PubMed=12477932;  
**RA** Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
**RA** Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
**RA** Altschul S.F., Zeeberg B., Butow R.H., Schaefer C.F., Bratt N.R.,  
**RA** Hopkins R.F., Jordan R., Moore T., Max S.I., Wang J., Hsieh F.,  
**RA** Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
**RA** Stapleton M., Soares M.B., Donaldson M.P., Casavant T.L., Scheetz T.E.,  
**RA** Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
**RA** Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullally S.J.,  
**RA** Bosak S.A., McEwan P.J., McFernan K.J., Malek J.A., Gunaratne P.H.,  
**RA** Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
**RA** Villalon D.K., Murphy D.M., Sodergren E.J., Lu X., Gibb R.A.,  
**RA** Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
**RA** Whiting M., Madan A., Young A.C., Shvchenko Y., Bouffard G.G.,  
**RA** Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
**RA** Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
**RA** Butterfield Y.S.N., Kryzwicki M.I., Skalska U., Smilus D.E.,  
**RA** Schmehl A., Schein J.E., Jones S.J.M., Marra M.A.;  
**RT** "Generation and initial analysis of more than 15,000 full-length  
**RT** human and mouse cDNA sequences.";  
**RL** Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
**RN** [5]
- RP SEQUENCE OF 22-36 AND 378-401.  
**RX** MEDLINE=98238645; PubMed=9571159;  
**RA** Tomoyasu A., Goto M., Fujise N., Mochizuki S.-I., Yasuda H.,  
**RA** Morinaga T., Tsuda E., Higashio K.;  
**RT** "Characterization of monomeric and homodimeric forms of  
**RT** osteoclastogenesis inhibitory factor".;  
**RL** Biochem. Biophys. Res. Commun. 245:382-387(1998).  
**RN** [6] [7]  
**RP** SEQUENCE OF 22-393 FROM N.A.  
**RC** TISSUE=Placenta;  
**RA** He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-P.;  
**RA** Tsuda E., Goto M., Mochizuki S.-I., Yano K., Kobayashi F.,  
**RA** Morinaga T., Higashio K.;  
**RT** "Isolation of a novel cytokine from human fibroblasts that  
**RT** specifically inhibits osteoclastogenesis.";  
**RL** Biochem. Biophys. Res. Commun. 234:137-142(1997).  
**RN** [8]  
**RP** TRAIL BINDING.  
**RA** Emery J.G., McDonnell P., Burke M.B., Deen K.C., Lyn S., Silverman C.,  
**RA** Dull B., Appelbaum E.R., Eichman C., DiPrinzio R., Dodds R.A.,  
**RA** James I.E., Rosenberg M., Lee J.C., Young P.R.,  
**RT** "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";  
**RL** J. Biol. Chem. 273:14363-14367(1998).  
**RN** [9]  
**RP** CHARACTERIZATION, AND MUTAGENESIS OF CYS-400.  
**RX** MEDLINE=98148058; PubMed=947964;  
**RA** Yamaguchi K., Kinosaki M., Goto M., Kobayashi F., Tsuda E.,  
**RA** Morinaga T., Higashio K.;  
**RT** "Characterization of structural domains of human osteoclastogenesis  
**RT** inhibitory factor.";  
**RL** J. Biol. Chem. 273:5117-5123(1998).  
**RN** [10]  
**RP** REVIEW.  
**RX** MEDLINE=21395914; PubMed=11505389;  
**RA** Hofbauer L.C., Neubauer A., Heufelder A.E.,  
**RT** "Receptor activator of nuclear factor-kappaB ligand and  
**RT** osteoprotegerin: potential implications for the pathogenesis and  
**RT** treatment of malignant bone diseases.";  
**CC** Cancer 92:460-470(2001).  
**CC** -1- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes  
**CC** its function in osteoclastogenesis. Inhibits the activation of  
**CC** osteoclasts and promotes osteoclast apoptosis in vitro. Bone  
**CC** homeostasis seems to depend on the local RANKL/OPG ratio. May also  
**CC** play a role in preventing arterial calcification. May act as decoy  
**CC** receptor for TRAIL and protect against apoptosis. TRAIL binding  
**CC** blocks the inhibition of osteoclastogenesis.  
**CC** -1- SUBUNIT: Homodimer.  
**CC** -1- SUBCELLULAR LOCATION: Secreted.  
**CC** -1- TISSUE SPECIFICITY: Highly expressed in adult lung, heart, kidney,  
**CC** liver, spleen, thymus, prostate, ovary, small intestine, thyroid,  
**CC** lymph node, trachea, adrenal gland, testis, and bone marrow.  
**CC** Detected at very low levels in brain, placenta and skeletal  
**CC** muscle. Highly expressed in fetal kidney, liver and lung.  
**CC** -1- INDUCTION: Upregulated by increasing calcium-concentration in the  
**CC** medium and estrogens. Downregulated by glucocorticoids.  
**CC** -1- PTM: N-glycosylated. Contains sialic acid residues.  
**CC** -1- PTM: The N-terminus is blocked.  
**CC** -1- SIMILARITY: Contains 4 TNFR-Cys repeats.  
**CC** -1- SIMILARITY: Contains 2 death domains.  
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**CC** modified and this statement is not removed. Usage by and for commercial  
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**CC** or send an email to license@isb-sib.ch).

		T11B RAT	STANDARD;	PRT;	401 AA.
ID	ID T11B RAT				
DR	EMBL; U94332; AAB53709.1; -.				
DR	EMBL; AB002146; BAA25910.1; -.				
DR	EMBL; AB008822; BAA32076.1; -.				
DR	EMBL; AB008815; BAA32076.1; JOINED.				
DR	EMBL; BC030155; AAF3155.1; -.				
DR	EMBL; AFI34187; AAF20168.1; -.				
DR	HSSP; P25542; ICDF.				
DR	Genew; HGNC:11909; TNFRSF1B.				
DR	NIM; 602633; -.				
DR	GO; GO:0005576; C:extracellular; TAS.				
DR	GO; GO:0005125; F:cytokine activity; TAS.				
DR	GO; GO:0004872; F:receptor activity; TAS.				
DR	GO; GO:000165; P:skeletal development; TAS.				
DR	GO; GO:0001501; P:skelatal development; TAS.				
DR	InterPro; IPR004486; Death.				
DR	InterPro; IPR001368; TNFR_C6.				
DR	Pfam; PF00020; TNFR_C6; 3.				
DR	SMART; SM0005; DEATH; 1.				
DR	SM0008; TNFR; 4.				
DR	PROSITE; PS50017; DEATH DOMAIN; FALSE_NEG.				
DR	PROSITE; PS50052; TNFR_NGFR; 1.				
DR	PROSITE; PS50050; TNFR_NGFR; 2; 2.				
KW	Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.				
FT	SIGNAL; 1; 21				
FT	CHAIN; 22; 401	TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B.			
FT	REPEAT; 24; 62	TNFR-CYS 1.			
FT	REPEAT; 65; 105	TNFR-CYS 2.			
FT	REPEAT; 107; 142	TNFR-CYS 3.			
FT	REPEAT; 145; 185	TNFR-CYS 4.			
FT	REPEAT; 198; 269	DEATH 1.			
FT	DOMAIN; 270; 365	DEATH 2.			
FT	SITE; 400; 400	INVOLVED IN DIMERIZATION.			
FT	DISULFID; 41; 54	BY SIMILARITY.			
FT	DISULFID; 44; 62	BY SIMILARITY.			
FT	DISULFID; 65; 80	BY SIMILARITY.			
FT	DISULFID; 83; 97	BY SIMILARITY.			
FT	DISULFID; 87; 105	BY SIMILARITY.			
FT	DISULFID; 107; 118	BY SIMILARITY.			
FT	DISULFID; 124; 142	BY SIMILARITY.			
FT	DISULFID; 145; 160	BY SIMILARITY.			
FT	DISULFID; 165; 185	BY SIMILARITY.			
FT	DISULFID; 198; 215	N-LINKED (GLCNAC. . . ) (POTENTIAL).			
FT	CARBODY; 152; 152	N-LINKED (GLCNAC. . . ) (POTENTIAL).			
FT	CARBODY; 165; 165	N-LINKED (GLCNAC. . . ) (POTENTIAL).			
FT	CARBODY; 178; 178	N-LINKED (GLCNAC. . . ) (POTENTIAL).			
FT	CARBODY; 289; 289	N-LINKED (GLCNAC. . . ) (POTENTIAL).			
FT	VARIANT; 3; 3	K->N. /FTIG-VAR 013439.			
FT	MUTAGEN; 400; 400	C--S: ABOLISHES DIMERIZATION.			
FT	MUTAGEN; 400; 401	MISSING: ABOLISHES DIMERIZATION.			
FT	MUTAGEN; 263; 263	D -> A (IN REF. 1).			
FT	SEQUENCE; 401 AA; 46040 MW;	EDR448B67D86C71E CRC54;			
Query	Match; 21; 1%; Score 239.5; DB 1; Length 401;				
Best	Local Similarity 30.9%; Pred. No. 1.7e-13;				
Matches	51; Conservative 21; Mismatches 84; Indels 9; Gaps 4;				
QY	25 EPOHKTCGSRPPTIVUSAKSRKIRITVCACTAENSNEHNNYLTCQLCRP-CDPVWGL	83			
QY	34 EFSHQQLDCDKPPTGTYIKQHCTAKWKVQCAPCDPHYTDSWHTSDCILYCSPVKELQVV	93			
QY	84 ERTPACTSKRKYQRCOPGMCAAWALECTHELLSDCOPPTAEALKDEVKGNNHCVPC	143			
QY	94 KQ--ECNRTHRNVRCECKEGRY---LEIEFLCKHRSCPPR-GIVQAGTERNVTKRC	145			
Db	144 KAGHPQTSSPSARCQHTRCENQGLYVAACTAQSTDTCKNPL	188			
QY	146 PDGFFSNETSSKAPCRKHTNCVFGLLITQKGNAUTHNICSGSE	190			
Db					
FT	CHAIN; 22; 401	TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B.			
FT	REPEAT; 24; 62	TNFR-CYS 1.			
FT	REPEAT; 65; 105	TNFR-CYS 2.			
FT	REPEAT; 107; 142	TNFR-CYS 3.			
FT	REPEAT; 145; 185	TNFR-CYS 4.			
FT	DOMAIN; 198; 269	DEATH 1.			
FT	DOMAIN; 270; 365	DEATH 2.			
FT	SITE; 400; 400	INVOLVED IN DIMERIZATION ( BY SIMILARITY).			
FT	DISULFID; 41; 54	BY SIMILARITY.			
FT	DISULFID; 44; 62	BY SIMILARITY.			
FT	DISULFID; 65; 80	BY SIMILARITY.			
FT	DISULFID; 83; 97	BY SIMILARITY.			
FT	DISULFID; 87; 105	BY SIMILARITY.			



PDB; 1JMA;	26-SEP-01.	DR
GeneID; HGNC:11912;	TNFRSF14.	DR
MIM; 602746;	-	DR
GO; GO:0005027;	F-NGF/INF (6 C-domain) receptor activity; TAS.	DR
GO; GO:0007166;	P; cell surface receptor linked signal transdu. . . ; TAS.	DR
GO; GO:0005955;	P-immune response; TAS.	DR
InterPro; IPR008053;	Fas receptor.	DR
InterPro; IPR01168;	TNFR_c6.	DR
PRINTS; PRO1680;	FASRECEPTOR.	DR
SMART; SM00208;	TNFR_3.	DR
PROSITE; PS00652;	TNFR_NGFR_1; 1.	KW
PROSITE; PS00500;	TNFR_NGFR_2; 1.	KW
Receptor; transmembrane;		KW
3D-structure.		KW
SIGNAL	1	FT
CHAIN	3	FT
FT	39	FT
FT	283	FT
FT	38	FT
FT	202	FT
FT	202	FT
FT	223	FT
FT	223	FT
FT	283	FT
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FT	135	FT
FT	120	FT
FT	110	FT
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FT	173	FT
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VARIANT	17	FT
VARIANT	241	FT
VARIANT	241	FT
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FT	124	FT
FT	125	FT
FT	125	FT
FT	140	FT
SEQUENCE	283 AA;	SQ
Query	20-3%; Score 230.5; DB 1; Length 283;	Match
Best Local Similarity	30.1%; Pred. No. 7.1e-13; Mismatches 66; Indels 51; Gaps 6;	Matches
Matches	56; Conservative 13; Mismatches 66; Indels 51; Gaps 6;	
QY	7 PPyASeNqTcRQDKQKEYYEPQRHtCCSRCPGTYSAKCSRIRDTCATCAENSYHNW	7
QY	89 GLSKLQOCMCDPAGMLRASRNCSRHENAVGCSPGHFC-----	33
Db	67 YLTICOLCRCPDPVGLEETAPCISKRKTCRCQPGMFCAWAHLCTCHCELLSBCPPGE	PCVAPLPSCN-EDEPY--PGSBCCPKCPGPGYRYKEACELGTSVCECPGGTYAHIN
Db	89 GLSKLQOCMCDPAGMLRASRNCSRHENAVGCSPGHFC-----	PCVAPLPSCN-EDEPY--PGSBCCPKCPGPGYRYKEACELGTSVCECPGGTYAHIN
Db	127 AFLKQEVGKGNNHCTPKASHFQNTSSPASRCQPHRCENOGVLNEAAPGIAQSDTICKNP	186
Db	128 -----IVQGDHCAACRA-----YATSSPQRQV-----KGCTESPDITCQ-	PDB
QY	187 LEPLPP	1
Db	165 --CPP	167
RESULT	15	
TR21_HUMAN		ID
TR21_HUMAN		TD
STANDARD		AC
PRT	655 AA.	DT
	07509; Q96DB6;	DT
	28-FEB-2003 (Rel. 41, Created)	DT
	28-FEB-2003 (Rel. 41, Last sequence update)	DT
	"Identifcation and functional characterization of DR6, a novel death receptor superfamily member 21 precursor (TNFR-related death receptor-6)"	DE
	Tumor necrosis factor receptor superfamily member 21 precursor (TNFR-related death receptor-6)	DE
	TNFRSF21 OR DRE	GN
	Homo sapiens (Human)	OS
	Bukay-Yoata, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC	OC
	Mammalia; Eutetaria; Primates; Catarrhini; Hominidae; Homo. OX	OX
	NCBI_TaxID=9605;	RN
	[1]	RP
	SEQUENCE FROM N.A.	RC
	MEDLINE=9337833; PubMed=9714541;	RX
	/FTId=VAR_013407.	RX
	V->I.	RX
	/FTId=VAR_013440.	RX
	SEQUENCE FROM N.A.	RP
	Parker A.; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.	RP
	[3]	RL
	SEQUENCE FROM N.A.	RP
	TISSUE=Brain, and Colon;	RC
	MEDLINE=22388257; PubMed=12477932;	RX
	Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,	RA
	Klauser R.D., Collins F.S., Wagner L., Schenman C.M., Schulter G.D.,	RA
	Altenschlager S.F., Zeeberg B.R., Buetow K.H., Schaefer C.F., Bhat N.K.,	RA
	Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	RA
	Dilatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	RA
	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	RA
	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	RA
	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,	RA
	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	RA
	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	RA
	Villalon D.K., Mizony D.M., Sodergren E.J., Lu X., Gibbs R.A.,	RA
	Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,	RA
	Whiting M., Madan A., Young A.C., Shvchenko Y., Bouffard G.G.,	RA
	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	RA
	Rodriguez A.C., Grimes J., Schmutz J., Myers R.M.,	RA
	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,	RA
	Schinner A., Schein J.E., Jones S.J.M., Marras W.A.,	RA
	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; RT	RT
	Proc. Natl. Acad. Sci. U.S.A. 99:16890-16903(2002).	RT
	FUNCTION: May activate NF-kappa-B and JNK and promote apoptosis.	CC
	-- SUBUNIT: Associates with TRAF.	CC
	-- SUBCELLULAR LOCATION: Type I membrane protein (Probable).	CC
	-- SUBCELLULAR LOCATION: Contains 4 TNFR-Cys repeats.	CC
	-- TISSUE SPECIFICITY: Highly expressed in heart, brain, Placenta, pancreas, lymph node, thymus and prostate. Detected at lower levels in lung, skeletal muscle, kidney, testis, uterus, small intestine, colon, spleen, bone marrow and fetal liver. Very low levels were found in adult liver and peripheral blood leukocytes.	CC
	-- SIMILARITY: Contains 4 TNFR-Cys repeats.	CC
	-- CAUTION: It is uncertain whether Met-1 or Met-25 is the initiator.	CC
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CC	CC	CC	CC
DR	DR	DR	DR
EMBL; AF06868; AAC34583.1; -.	EMBL; AL096801; CAB75692.1; -.	EMBL; BC017730; AAH17730.1; -.	EMBL; BC010241; AAH10241.1; ALT_INIT.
DR	DR	DR	DR
HSSP; 014763; 1DOG.	MIM; 605732; -.	InterPro; IPR00488; Death.	InterPro; IPR001368; TNFR_c6.
DR	DR	DR	DR
Pfam; PF00020; TNFR_c6; 4.	SMART; SM00005; DEATH; 1..	PROSITE; PS00652; DEATH DOMAIN; 1..	PROSITE; PS00050; TNFR_NGFR_2; 1..
KW	KW	KW	KW
Receptor; Adoption; Transmembrane; Glycoprotein; Repeat; Signal.			
FT	FT	FT	FT
CHAIN	42	655	42
DOMAIN	42	349	350
TRANSMEM	350	370	370
FT	FT	FT	FT
DOMAIN	371	655	415
FT	FT	FT	FT
DOMAIN	415	498	50
FT	FT	FT	FT
REPEAT	88	88	90
FT	FT	FT	FT
REPEAT	90	131	131
FT	FT	FT	FT
REPEAT	133	167	170
FT	FT	FT	FT
REPEAT	170	211	211
FT	FT	FT	FT
DISULFID	67	80	70
FT	FT	FT	FT
DISULFID	70	88	91
FT	FT	FT	FT
DISULFID	91	105	109
FT	FT	FT	FT
DISULFID	109	123	113
FT	FT	FT	FT
DISULFID	113	131	133
FT	FT	FT	FT
DISULFID	133	144	150
FT	FT	FT	FT
DISULFID	150	168	171
FT	FT	FT	FT
DISULFID	168	186	186
FT	FT	FT	FT
DISULFID	171	192	192
FT	FT	FT	FT
CARBONYD	192	211	82
FT	FT	FT	FT
CARBONYD	82	82	141
FT	FT	FT	FT
CARBONYD	141	141	141
FT	FT	FT	FT
CARBONYD	141	252	252
FT	FT	FT	FT
CARBONYD	252	257	257
FT	FT	FT	FT
CARBONYD	257	278	278
FT	FT	FT	FT
CARBONYD	278	289	289
FT	FT	FT	FT
SEQUENCE	289	655 AA;	71844 MW;
Query	Match	Best Local Similarity	Score
Qy	Matches	56;	20.2%;
Db	Qy	Conservative	228.5;
Db	Qy	56;	Score
Db	Qy	Mismatches	DB 1;
Db	Qy	30	Length
Db	Qy	ICCSRPPGTIVSAKSRIRDTWCATCAENSNEHNNYLTICQLC-RPCDPVNGLEIAP	65
Db	Qy	LTCDKPQAGTYSERCHNTSRSVCSSCP-VGFTTRHENGIEKRDSCPC-PFMMEKL-P	89
Db	Qy	CTSKRKRQCRQPGMF---CAAWALECTHCELLSSCP-----IGTEAULKDEVGKG	123
Db	Qy	137 NNHCYVCKAGHQNTTSPSAQPHRCENQCLVERARGIAQSDTAKPLPPEMSG	164
Db	Qy	165 DVCCKOCARGTFSDVPSVSSVMCKAYTDCLSONLWVKPGTKETDNVCGT---LPSFSS	196
Qy	197 T 197	221 T 221	220

Search completed: August 28, 2004, 01:49:30  
Job time : 26 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

## OM protein - protein search, using SW model

Run on: August 28, 2004, 01:31:38 ; search time 115 Seconds

(without alignments)  
540.496 Million cell updates/sec

Title: us-10-003-211-1  
Perfect score: 1133  
Sequence: 1 SQPQAVPPYASENQTCRDQE.....QSDTCKNPLRPLPPEMSGT 197

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPREMBL\_25; \*

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

SPREMBL\_25; \*

1: sp\_archea: \*  
2: sp\_bacteria: \*  
3: sp\_fungi: \*  
4: sp\_human: \*  
5: sp\_invertebrate: \*  
6: sp\_mammal: \*  
7: sp\_inhc: \*  
8: sp\_organelle: \*  
9: sp\_phage: \*  
10: sp\_plant: \*  
11: sp Rodent: \*  
12: sp\_virus: \*  
13: sp\_vertebrate: \*  
14: sp\_unclassified: \*  
15: sp\_rvirus: \*  
16: sp\_bacteriap: \*  
17: sp\_archeap: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No. Score % Query Length DB ID Description

Result No.	Score	%	Query	Length	DB	ID	Description
1	309.5	27.3	483	13	Q800K7	Q800K7 paralichthys olivaceus	Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
2	295.5	26.1	278	6	Q85Q34	Q85Q34 sus scrofa	DR GO; GO:0004872; F-receptor activity; IEA.
3	291.5	25.7	433	11	Q91LM6	Q91LM6 rattus norvegicus	DR Int-PRO; IPR01168; TNFR_c6.
4	291.5	25.7	474	11	Q80W16	Q80W16 rattus norvegicus	DR PROTEIN; PFO0020; TNFR_c6; 3.
5	290	25.6	459	11	Q62327	Q62327 mus musculus	DR SMART; SM00208; TNFR_4.
6	284.5	25.1	274	6	Q7YR15	Q7YR15 canis familiaris	DR PROSITE; PS00652; TNFR_NGFR_1; 1.
7	278	24.5	223	4	Q86YK5	Q86YK5 homo sapiens	DR PROSITE; PSS0050; TNFR_NGFR_2; 3.
8	276.5	24.4	482	11	Q88734	Q88734 mus musculus	KW Receptor.
9	265.5	23.4	277	6	Q8WM02	Q8WM02 ovis aries	SQ SEQUENCE.
10	258	22.8	275	11	Q80W19	Q80W19 mus musculus	Query Match Best Local Similarity 27.3%; Score 309.5; DB 13; Length 483; Matches 64; Conservative 20; Mismatches 80; Indels 17; Gaps 6;
11	253	22.3	462	13	Q805B0	Q805B0 gallus gallus	DR Q8K226 mus musculus
12	243.5	21.5	289	11	Q8K2X6	Q8K2X6 cercopithecus aethiops	DR Q8KEZ8 cercopithecus aethiops
13	242.5	21.4	283	6	Q9X528	Q9X528 cowpox virus	DR Q7T2J5 cowpox virus
14	240	21.2	186	12	Q7T2J5	Q7T2J5 onychomycosis virus	DR Q9PU50 salvelinus
15	238.5	21.1	318	13	Q7T2H3	Q7T2H3 onychomycosis virus	DR Q9PU50 salvelinus
16	238	21.0	302	13	Q9PU50	Q9PU50 salvelinus	DR Q9PU50 salvelinus

Database : SPREMBL\_25; \*

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

SPREMBL\_25; \*

1: sp\_archea: \*  
2: sp\_bacteria: \*  
3: sp\_fungi: \*  
4: sp\_human: \*  
5: sp\_invertebrate: \*  
6: sp\_mammal: \*  
7: sp\_inhc: \*  
8: sp\_organelle: \*  
9: sp\_phage: \*  
10: sp\_plant: \*  
11: sp\_Rodent: \*  
12: sp\_virus: \*  
13: sp\_vertebrate: \*  
14: sp\_unclassified: \*  
15: sp\_rvirus: \*  
16: sp\_bacteriap: \*  
17: sp\_archeap: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## ALIGNMENTS

17	233.5	20.6	457	4	Q8IVS6	Q8ivs6 homo sapien
18	232.5	20.5	467	13	Q80010	Q80010 gallus gallus
19	230	20.3	276	13	Q9DDd2	Q9Dd2 gallus gallus
20	230	20.3	351	12	Q57117	Q57117 cowpox virus
21	229.5	20.3	285	13	Q90W71	Q90W71 oncornyvirus
22	226.5	20.0	167	12	Q8UYI3	Q8uyi3 vaccinia virus
23	225.5	19.9	186	13	Q7ZZY5	Q7zz5 gallus gallus
24	225.5	19.9	651	13	Q98SM6	Q98sm6 oncornyvirus
25	225	19.9	186	12	Q9YPB7	Q9yp7 cowpox virus
26	225	19.9	349	12	Q57099	Q57099 monkeypox virus
27	225	19.9	349	12	Q57098	Q57098 camelpox virus
28	225	19.9	349	12	Q57284	Q57284 camelpox virus
29	223	19.7	186	12	Q911R5	Q911r5 vaccinia virus
30	221.5	19.5	285	13	Q9YS66	Q9yS66 oncornyvirus
31	221	19.5	349	12	Q57100	Q57100 monkeypox virus
32	221	19.5	349	12	Q57097	Q57097 camelpox virus
33	220.5	19.5	169	11	Q9JK80	Q9jke0 rattus norvegicus
34	219	19.3	349	12	Q57102	Q57102 monkeypox virus
35	219	19.3	349	12	Q57291	Q57291 monkeypox virus
36	218.5	19.3	167	12	Q9DJU2	Q9djU2 cowpox virus
37	218.5	19.3	350	12	Q57116	Q57116 cowpox virus
38	218	19.2	186	12	Q9WJB4	Q9wjB4 vaccinia virus
39	218	19.2	348	12	Q57108	Q57108 monkeypox virus
40	218	19.2	348	12	Q57103	Q57103 monkeypox virus
41	217.5	19.2	267	6	Q02764	Q02764 orctolagus cuniculus
42	216.5	19.1	167	12	Q72162	Q72162 cowpox virus
43	216	19.1	348	12	Q52777	Q52777 monkeypox virus
44	216	19.1	349	12	Q57101	Q57101 monkeypox virus
45	210	18.5	348	12	Q57112	Q57112 variola virus

**RESULT 2**

Q8SQ34 PRELIMINARY; PRT; 278 AA.

ID Q8SQ34; PRELIMINARY; PRT; 278 AA.

AC Q8SQ34; PRELIMINARY; PRT; 278 AA.

DT 01-JUN-2002 (TREMBrel. 21, Created)

DT 01-JUN-2003 (TREMBrel. 24, Last sequence update)

DE CD40.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI\_TAXID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RA West K.A., Li A.W.; Rowden G.;

RT "Characterization of the Porcine CD40 Molecule.";

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AR248545; AXL92941; -.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:004888; F:transmembrane receptor activity; IEA.

DR GO; GO:006915; P:apoptosis; IEA.

DR GO; GO:006955; P:immune response; IEA.

DR GO; GO:007165; P:signal transduction; IEA.

DR InterPro; IPR00863; TNFR\_c6.

DR Pfam; PF0020; TNFR\_c6.

DR PRINS; PR01680; FASRECEPTOR.

DR SMART; SM0208; TNFR\_NGFR\_4.

DR PROSITE; PS50050; TNFR\_NGFR\_1; 1.

DR PROSITE; PS50050; TNFR\_NGFR\_2; 4.

SQ SEQUENCE 278 AA; 30951 MW; 20D46E4AF93DD2 CRC64;

Query Match Best Local Similarity 26.1%; Score 295.5; DB 6; Length 278; Matches 62; Conservative 19; Mismatches 74; Indels 13; Gaps 3;

Best Local Similarity 36.9%; Pred. No. 5.4e-24; Score 295.5; DB 6; Length 278; Matches 62; Conservative 19; Mismatches 74; Indels 13; Gaps 3;

QY 21 KRYYEROHRICSRCPGTYVAKSRSRIRDTCATCAENSYNEHMLYLTCQLCRPCDPV 80

Db 27 KENQYPTINSRCSNLCPGQKVNHCYEVTECLCSSEFLATWNREKHQHQKYCDPN 86

QY 81 MGLIEETAPCTSKRKTKORCQCPMFCAAWALEBETHCELLSDQPPG----TAAELKDEVK 135

Db 87 LGLQVOREGTSKDTTVCSEGHCTNSA-GESCTHSLSLPPGLGWQMATEVSTI-- 142

QY 136 GMNHCVCKAARFQNTSSPSARCOPHRCEVQGLVBAQPGTAQSDTC 183

Db 143 ---CEPCPVGFNSVSSASEKQPMWTSCESKGLVEORAGTNKIDWVC 186

RESULT 3

Q91ZM6 PRELIMINARY; PRT; 433 AA.

ID Q91ZM6; PRELIMINARY; PRT; 433 AA.

AC Q91ZM6; PRELIMINARY; PRT; 433 AA.

DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)

DE Tumor necrosis factor receptor type II (Fragment).

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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**RESULT 4**

Q80W76 PRELIMINARY; PRT; 474 AA.

ID Q80W76; PRELIMINARY; PRT; 474 AA.

AC Q80W76; PRELIMINARY; PRT; 474 AA.

DT 01-JUN-2003 (TREMBrel. 24, Last sequence update)

DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)

DE Tumor necrosis factor receptor type II.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TAXID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Wistar; TISSUE=spleen;

RA Li Y., Ji A., Schafer M.K.;

RT "Expression of TNFR2 in rat dorsal root ganglion.";

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF498039; AAP3151\_1;

DR GO; GO:004872; F:receptor activity; IEA.

DR InterPro; IPR001368; TNFR\_c6.

DR Pfam; PF00020; TNFR\_c6; 4.

DR SMART; SM00208; TNFR\_4.

DR PROSITE; PS50052; TNFR\_NGFR\_1; 2.

DR PROSITE; PS50050; TNFR\_NGFR\_2; 3.

DR Receptor.

SQ SEQUENCE 474 AA; 50148 MW; 298C6AB9E8C8D714 CRC64;

Query Match Best Local Similarity 33.3%; Score 291.5; DB 11; Length 474;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TAXID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley;

RA Osburg B., Peiser C., Doenling D., Schomburg L., Voigt K., Bickel U.;

RT "TNF-receptors p60 and p80 are constitutively expressed by rat brain capillary endothelial cells and participate in TNF-alpha transport through the blood-brain barrier.";

RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF420214; ALU16021\_1;

DR GO; GO:004872; F:receptor activity; IEA.

DR InterPro; IPR001368; TNFR\_c6.

DR Pfam; PF00020; TNFR\_c6; 4.

DR SMART; SM00208; TNFR\_c6.

DR PROSITE; PS50052; TNFR\_NGFR\_1; 2.

DR PROSITE; PS50050; TNFR\_NGFR\_2; 3.

DR Receptor.

FT NON\_TER 1 1

FT NON\_TER 433 AA; 433 MW; 75736B835E72CA4A CRC64;

SQ SEQUENCE 433 AA; 45723 MW; 75736B835E72CA4A CRC64;

Query Match Best Local Similarity 25.7%; Score 291.5; DB 11; Length 433; Matches 65; Conservative 24; Mismatches 91; Indels 15; Gaps 7;

QY 8 PYASENQTCRDQEKEYYEPHRITCCSRPDPGTYSVAKSRSIRDTCATCAENSYHNWY 67

Db 11 PYKPERPGNCQKISOEYDVKKAQMCACKPGQVAKHFCKMTSDTCVCAAGHFTQVNHH 70

QY 68 LTICOLC-RPC--DPYVMGLERIAEPTSKRKTKORCQCPMFCAAWALEBETHCELLSDQ 122

Db 71 LHTCUCSSSCSDDDQV---ETHNCTKQNRVCAACNAADSYCALKLHSNGRCQCMKLSKG 126

QY 123 PGTEAELKDEVKGKNNHCVPKAGHFQNTSSPSARCOPTRCENQGLVRAAPGTAQSPRT 182

Db 127 PGF-GVARARTSNGVIVSACAPGTFPSDTTSSTDVCRPHRCS---IIAIPGNASIDAV 181

QY 183 CKNPLBLPLPEMMSGT 197

Db 182 CASE-SPTPSAVPRT 195



KW	Receptor.	SEQUENCE.	482 AA;	51106 MW;	F6C15046B48FF83C CRC64;
SQ					
Query Match	24.4%; Score 276.5; DB 11; Length 482;				
Best Local Similarity	32.3%; Pred. No. 1.1e-21; Mismatches 85; Indels 27; Gaps 9;				
Matches	65; Conservative 24; Mismatches 85; Indels 27; Gaps 9;				
Qy	8 PYASE-NOTCRDQBEKEYVEPQRICCSRCRPPGTIVSAKCSR1-----RDTCATCAEN 59				
Db	31 PYKEPEPGYECQISQ-EYDRKQAMCCAKCPcQPVYKHFCKNKUSDTWDVACADSPTVACDEAS 89				
Qy	60 SYNEHWMLVLTQOLR---PCPVMGLHETIAPTSKRTQCRQGPNFCA--AWALEETH 114				
Db	90 MYTQWQNFQRTCLSCSSCSTDQV---ETRACTKQONRVCAEAGRYCALKHSGSRQ 145				
Qy	115 CELSIDPPGTEAKLKGKVNGKNNHCVPKASHFONTSSPSARCPHRCENCNGIVEAAP 174				
Db	146 CMRLSKCQPF-GVASSRAPGVNLKACAPGFDSTTSIDVCRPHICS---ILAIPI 200				
Qy	175 GTAQSDTTCKNPLEPLPEMS 195				
Db	201 GNASTDAVC---APESTLS 217				
RESULT 8					
ID	OBMMQ2	PRELIMINARY;	PRT;	277 AA.	
AC	OBMMQ2;				
DT	01-MAR-2002 (TREMBlrel. 20, Last sequence update)				
DT	01-JUN-2003 (TREMBlrel. 24, Last annotation update)				
Qy	67 YLTICQLCERPODPVNGLEETAPCTSKRKVQCRQPMFCAAWALECTHCELLSDCPGPGE 126				
Db	73 RETICHQHKVCPNGLRIVQQKGHSETDTCTCERGWHTCNSSEA--CESCVLHRSCSPGFG 130				
Qy	127 AELKDEVGKGNHCVPKACKFHONTSSPSARCPHTRCENQGLIVEAHPQAQSITC 183				
Db	131 VK-QIATGVSDTICECPCPVGFNSNVSAFEKHPATCERKDVWQAGTNKTBVVC 186				
RESULT 9					
ID	QBMMQ2	PRELIMINARY;	PRT;	277 AA.	
AC	QBMMQ2;				
DT	01-MAR-2002 (TREMBlrel. 20, Last sequence update)				
DT	01-JUN-2003 (TREMBlrel. 24, Last annotation update)				
Qy	146 CMLSKCQPF-GVASSRAPGVNLKACAPGFDSTTSIDVCRPHICS---ILAIPI 200				
Db	175 GTAQSDTTCKNPLEPLPEMS 195				
Qy	201 GNASTDAVC---APESTLS 217				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Zawitkowsk M.S., Russ G.R., Krishnan R.;				
RT	"Cloning and expression of the ovine CD40 molecule and the inhibition of the mixed lymphocyte reaction by the ovine CD40-EGFP fusion protein.",				
RT	Submitted (JAN 2002) to the EMBL/GenBank/DDBJ databases.				
RL	AY072798; AAU68402; I;				
DR	EMBL; AY072798; AAU68402; I;				
DR	GO; GO_0016020; C:membrane; IEA.				
DR	GO; GO_000888; F:transmembrane receptor activity; IEA.				
DR	GO; GO_000915; P:apoptosis; IEA.				
DR	GO; GO_0006955; P:immune response; IEA.				
DR	GO; GO_007165; P:signal transduction; IEA.				
DR	InterPro; IPR001368; TNFR_c6.				
DR	PFAM; PF00020; TNFR_c6; 4.				
DR	PRINTS; PR01680; FASRECEPTOR.				
DR	SMART; SM00208; TNFR; 4.				
DR	PROSITE; PS00152; TNFR_NGFR_1; 1.				
DR	PROSITE; PS00050; TNFR_NGFR_2; 1.				
FT	NON TER 277 277				
SQ	SEQUENCE 277 AA; 30465 MW; 619F28BEA1BA0D29 CRC64;				
Query Match	23.4%; Score 265.5; DB 6; Length 277;				
Best Local Similarity	33.7%; Pred. No. 1e-20; Mismatches 80; Indels 9; Gaps 4;				
Matches	56; Conservative 21; Mismatches 80; Indels 9; Gaps 4;				
Qy	20 EKEYEEQHRCCSRCPGTVYSAKCSRIRDTVCATCAENSYEHMAYLTICQLCPCDP 79				
Db	28 EKQY-PVNSLCDCDLCPGQKLNDCTEVSKKRCQSGKGEFLSTMRREKYCHEHRVNP 85				
Qy	80 VMGLEEAPCTSRSKRKQRCQPMFCAAWALECTHCELLSDCPGPGEAEKDEVGK3-N 137				
Db	86 NLGLRIQSEGNTDTTCVCDQGHCSTH---CESCPHSLCLPGFGVK---QIATGVLD 140				
Qy	138 NHCVPKACKFHONTSSPSARCPHTRCENQGLIVEAHPQAQSITC 183				

Db 141 TICERCPVGFNSVSSAFKCHPWTSCRKGLIVEQHVGTKNDAVC 186  
 RESULT 10  
 Q80WM9 PRELIMINARY; PRT; 275 AA.  
 ID Q80WM9  
 AC Q80WM9;  
 DT 01-JUN-2003 ('TREMBLrel. 24, Created)  
 DT 01-JUN-2003 ('TREMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 ('TREMBLrel. 25, Last annotation update)  
 DB Tumor necrosis factor receptor superfamily member 14 precursor.  
 OS Mus musculus (Mouse);  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;  
 NCBI\_TaxID=10090;  
 RN [1] \_SEQUENCE FROM N.A.  
 RP STRAIN=C5BL6; TISSUE=Thymus;  
 RA Benencia F., Conejo-Garcia J.R., Courreges M.C., Coukos G.;  
 RT "Light regulation in a murine model of ovarian carcinoma.";  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL: AY264405; AACB09081\_1;  
 GO; GO: 001620; C:membrane; IEA.  
 DR GO; GO: 0004888; P:transmembrane receptor activity; IEA.  
 DR GO; GO: 0006915; P:apoptosis; IEA.  
 DR GO; GO: 0006955; P:immune response; IEA.  
 DR SMART; SW0208; TNFR\_4;  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 3.  
 DR InterPro; IPR01368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_C6; 4.  
 DR PRINTS; PR0180; FASRECEPTOR.  
 DR SMART; SW0208; TNFR\_4;  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 3.  
 KW Receptor; Signal; FT SIGNAL 1 38  
 SEQUENCE 275 AA; 30171 MW; C47EAR8EFC0521D CRC64;  
 Query Match 22.8%; Score 258; DB 11; Length 275;  
 Best Local Similarity 34.6%; Pred. No. 6..6-20;  
 Matches 63; Conservative 14; Mismatches 86; Indels 18; Gaps 6;  
 Db 37 SAQPSCRQBFVLGDE--CCPMCNPGHVQKVSEHTGTVCACPPOVYTAHNGSK 92  
 Qy 7.1 CQLGRPCPDYVGLBIAPIRTSKRTQCRQPGMCAAWALECTHCELLSDCPGTAEAL 129  
 93 CLPGGVCDPDMGLTWOQECSSWQDKTVCRCQIPIGYCENODGSHCSTCLDTTCPGQRYEV- 151  
 Qy 130 KDEVGKGNM-----CVPKAGHQNTSSPSARQPHRCGTCENQGLIVEAARGTAQSDTTCK 184  
 Db 152 -----KRGHHDQPTVCADLITGF-SLGQTQEECLPWTNC-SAFQKEVRGINSIDTCS 204  
 Qy 185 N 185  
 Db 205 S 205  
 RESULT 11  
 Q805B0 PRELIMINARY; PRT; 462 AA.  
 ID Q805B0  
 AC Q805B0;  
 DT 01-JUN-2003 ('TREMBLrel. 24, Created)  
 DT 01-JUN-2003 ('TREMBLrel. 25, Last annotation update)  
 DE Tumor necrosis factor receptor-II.  
 DE Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 GN TNFR-II.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus. OX NCBI\_TaxID=9031;  
 RN [1] \_SEQUENCE FROM N.A.  
 RP STRAIN=White leghorn H-B15; TISSUE=Spleen;  
 RA Sayde A.A.; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.  
 RN [2] \_SEQUENCE FROM N.A.  
 RP STRAIN=White leghorn H-B15; TISSUE=Spleen;  
 RA Sayde A.A.; Horuchi H., Furusawa S., Matsuda H.;  
 RT Molecular cloning and characterization of chicken Tumor necrosis factor receptor-II (TNFR-II) and Tumor necrosis factor receptor-associated factor-5 (TRAF-5) genes.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL: AB101004; AACB5965.1; -.  
 DR GO; GO: 0016020; C:membrane; IEA.  
 DR GO; GO: 0004888; P:transmembrane receptor activity; IEA.  
 DR GO; GO: 0006955; P:immune response; IEA.  
 DR GO; GO: 0007165; P:signal transduction; IEA.  
 DR InterPro; IPR01368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_C6; 3.  
 DR PRINTS; PR01680; FASRECEPTOR.  
 DR SMART; SW0208; TNFR\_4;  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 3.  
 KW Receptor; Sequence; FT SIGNAL 1 38  
 SEQUENCE 275 AA; 30171 MW; C47EAR8EFC0521D CRC64;  
 Query Match 22.3%; Score 253; DB 13; Length 462;  
 Best Local Similarity 29.4%; Pred. No. 3..9e-19;  
 Matches 59; Conservative 24; Mismatches 100; Indels 18; Gaps 6;  
 Db 8 PYASHEQNQTRDQEKEYYEQHRIICSRCCRGTCYVSAKCSRIRDVCATCAENSYEHWN 67  
 Qy 23 PYTPOSAOCRNPSFTEYYEERLKKCQSKCPCGQKRAESGSHSVDTKCIPCLPDTVTAWN 82  
 Db 68 LITIQQLCR-PCDPVNGLERIAPCTSSKRKTQCRCOFGMFCAAWALE-CTHCELLSDCPGT 125  
 83 SPQCFCASPCR-KGFWENQNTCTLSWDRICSCPCPNYCISKMYQNCCHICKVHKKGGRY 140  
 Qy 126 EAELKDEVGKGNHICVPCKGHTQNTSSPSARQPHRCGTCENQGLIVEAARGTAQSDTTCK 185  
 Db 141 RVSRRG-TDSTDTECKPCPGTFSDEESYDTSCIFHTVCKS---VAVAGNNVNIDTVCHO 195  
 Qy 186 PLEP-----LPPEMGAT 197  
 Db 196 SVATLPHFTAVNLFQSST 216  
 RESULT 12  
 Q8KZK6 PRELIMINARY; PRT; 289 AA.  
 ID Q8KZK6  
 AC Q8KZK6;  
 DT 01-OCT-2002 ('TREMBLrel. 22, Created)  
 DT 01-OCT-2002 ('TREMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 ('TREMBLrel. 25, Last annotation update)  
 DB Similar to tumor necrosis factor receptor superfamily, member 5.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1] \_SEQUENCE FROM N.A.  
 RP STRASBURG R.; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 RA STRASBURG R.; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 RL EMBL: BC029254; AAH29254.1; -.  
 DR GO; GO: 0016020; C:membrane; IEA.  
 DR GO; GO: 0005634; C:nucleus; IEA.  
 DR GO; GO: 0005640; C:ribosome; IEA.  
 DR GO; GO: 0003677; P:DNA binding; IEA.  
 DR GO; GO: 0003735; P:structural constituent of ribosome; IEA.

DR	GO; GO:0004888; F:transmembrane receptor activity; IEA.	SQ	SEQUENCE 283 AA; 30199 MW; 397951C6617FEEAA CRC64;
DR	GO; GO:000915; P:apoptosis; IEA.	Query Match	21.4%; Score 242.5; DB 6; Length 283;
DR	GO; GO:000955; P:immune response; IEA.	Best Local Similarity	32.2%; Pred. No. 3; e-18;
DR	GO; GO:000612; P:protein biosynthesis; IEA.	Matches	57; Conservative 18; Mismatches 85; Indels 17; Gaps 6;
DR	GO; GO:000165; P:signal transduction; IEA.	QY	9 YASENOTCRDQEKEYVYBHQHRCCSRPPGTVYSAKSRIRPWCATCAENSYNEHWYL 68
DR	InterPro; IPR008063; Fas receptor.	DB	15 TICOLCRCDPVMGLEELAPCTSRRKTQCORCQGMFCAW-ALECTHECELLSDCPPEA 127
DR	InterPro; IPR001005; Myb_DNA binding.	Db	35 YAPALPSCK--EDEY--PGVSICCPKQGPFGHVQACGEGOTGVCEPCSPGTIAHNGL 90
DR	InterPro; IPR001368; TNFR_c6.	QY	69 TICOLCRCDPVMGLEELAPCTSRRKTQCORCQGMFCAW-ALECTHECELLSDCPPEA 127
DR	PRINTS; PR01680; FASRECEPTOR.	DR	91 SKCLOCQCMDPAMGLRTSRNSCTANALGCGCSPGHFCITQDGPHCAACRAYATSSPG-- 147
DR	SMART; SM00208; TNFR_4.	Do	128 ELKDEEVGGNNH---CVPKCAGHFONTSSPSARCOHTRCENQGLVEAAPGTAQS 179
DR	PROSITE; PS000962; RIBOSOMAL_S2_1.	QY	130 KDEVKGKNNHCPVKAGHFONTSSPSARCOHPHRCEENDGIVLEAAMPQAQSRTC 183
DR	PROSITE; PS00652; TNFR_NGFR_1; 1.	Db	139 TDTV-----CHPCPVGFSSNQSLFEKCYPWTSCEDKNLLEVLOKGTSINVIC 186
DR	PROSITE; PS00505; TNFR_NGFR_2; 4.	Do	148 --QRVQKGTESQDTLQNCPGTF-SSTNGTLEECOHNKCSKWLVEAGPOTISS 200
KW	Receptor.	SQ	SEQUENCE 289 AA; 32077 MW; DBE93B1E439F1E2A CRC64;
RESULT	13	Query Match	21.5%; Score 243.5; DB 11; Length 289;
Q9XSZ8	PRELIMINARY; PRT; 283 AA.	Best Local Similarity	31.0%; Pred. No. 2; Mismatches 81; Indels 17; Gaps 5;
ID	Q9XSZ8	Matches	54; Conservative 22; Mismatches 22; Indels 17; Gaps 5;
AC	Q9XSZ8;	QY	15 TCRDQEKEYVYBHQHRCCSRPPGTVYSAKSRIRPWCATCAENSYNEHWYL 74
DT	01-NOV-1999 (TREMBlrel. 12, Last sequence update)	DB	25 TCSD--KQYLHDGQ--CCDCIQPSRSLTSHCATLKPTQCHPUSGEFSAQWNWRBIRCHH 80
DT	01-JUN-2003 (TREMBlrel. 24, Last annotation update)	QY	75 RCPDPVMGLEELAPCTSRRKTQCORCQGMFCAW-ALECTHECELLSDCPPEA 129
DE	ASGR protein.	Db	81 RHCFENQGLRKVKGTAESDITVACKEGQCT--SKDCEACAGHTPCIPGFWEMATE 138
GN		QY	130 KDEVKGKNNHCPVKAGHFONTSSPSARCOHPHRCEENDGIVLEAAMPQAQSRTC 183
OS	Coxopx virus (CPV).	Db	139 TDTV-----CHPCPVGFSSNQSLFEKCYPWTSCEDKNLLEVLOKGTSINVIC 186
OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;	Do	148 --QRVQKGTESQDTLQNCPGTF-SSTNGTLEECOHNKCSKWLVEAGPOTISS 200
OX	Orthopoxvirus	Do	91 SKCLOCQCMDPAMGLRTSRNSCTANALGCGCSPGHFCITQDGPHCAACRAYATSSPG-- 147
NCBI_TAXID=10243;	QY	128 ELKDEEVGGNNH---CVPKCAGHFONTSSPSARCOHTRCENQGLVEAAPGTAQS 179	
RN	[1]	QY	130 KDEVKGKNNHCPVKAGHFONTSSPSARCOHPHRCEENDGIVLEAAMPQAQSRTC 183
RP	SEQUENCE FROM N.A.	Db	139 TDTV-----CHPCPVGFSSNQSLFEKCYPWTSCEDKNLLEVLOKGTSINVIC 186
RC	STRAIN=GRI-90; PubMed=9568042;	Do	148 --QRVQKGTESQDTLQNCPGTF-SSTNGTLEECOHNKCSKWLVEAGPOTISS 200
RA	Shchelkunov S.N., Safronov P.F., Totmenin A.V., Petrov N.A.,	Do	91 SKCLOCQCMDPAMGLRTSRNSCTANALGCGCSPGHFCITQDGPHCAACRAYATSSPG-- 147
RA	Riazankina O.I., Gutorov V.V., Kotwal G.J.;	Do	128 ELKDEEVGGNNH---CVPKCAGHFONTSSPSARCOHTRCENQGLVEAAPGTAQS 179
RT	"Species-specific differences in genome organization of cowpox,	Do	130 KDEVKGKNNHCPVKAGHFONTSSPSARCOHPHRCEENDGIVLEAAMPQAQSRTC 183
RT	smallpox, and vaccinia viruses."	Do	139 TDTV-----CHPCPVGFSSNQSLFEKCYPWTSCEDKNLLEVLOKGTSINVIC 186
RL	Virology 243:432-460 (1998).	Do	148 --QRVQKGTESQDTLQNCPGTF-SSTNGTLEECOHNKCSKWLVEAGPOTISS 200
RN	[2]	Do	91 SKCLOCQCMDPAMGLRTSRNSCTANALGCGCSPGHFCITQDGPHCAACRAYATSSPG-- 147
RP	SEQUENCE FROM N.A.	Do	128 ELKDEEVGGNNH---CVPKCAGHFONTSSPSARCOHTRCENQGLVEAAPGTAQS 179
RC	STRAIN=GRI-90;	Do	130 KDEVKGKNNHCPVKAGHFONTSSPSARCOHPHRCEENDGIVLEAAMPQAQSRTC 183
RX	PubMed=8963248;	Do	139 TDTV-----CHPCPVGFSSNQSLFEKCYPWTSCEDKNLLEVLOKGTSINVIC 186
RA	MEDLINE=97068532; PubMed=8963248;	Do	148 --QRVQKGTESQDTLQNCPGTF-SSTNGTLEECOHNKCSKWLVEAGPOTISS 200
RA	Safronov P.F., Petrov N.A., Riazankina O.I., Totmenin A.V.,	Do	91 SKCLOCQCMDPAMGLRTSRNSCTANALGCGCSPGHFCITQDGPHCAACRAYATSSPG-- 147
RA	Shchelkunov S.N., Sandakhev L.S.;	Do	128 ELKDEEVGGNNH---CVPKCAGHFONTSSPSARCOHTRCENQGLVEAAPGTAQS 179
RA	Shchelkunov S.N.,' Sandakhev L.S.;	Do	130 KDEVKGKNNHCPVKAGHFONTSSPSARCOHPHRCEENDGIVLEAAMPQAQSRTC 183
RT	Genes of a circle of hosts for the cowpox virus.";	Do	139 TDTV-----CHPCPVGFSSNQSLFEKCYPWTSCEDKNLLEVLOKGTSINVIC 186
RL	Dokl. Akad. Nauk 349:829-833 (1996).	Do	148 --QRVQKGTESQDTLQNCPGTF-SSTNGTLEECOHNKCSKWLVEAGPOTISS 200
RN	[3]	Do	91 SKCLOCQCMDPAMGLRTSRNSCTANALGCGCSPGHFCITQDGPHCAACRAYATSSPG-- 147
RP	SEQUENCE FROM N.A.	Do	128 ELKDEEVGGNNH---CVPKCAGHFONTSSPSARCOHTRCENQGLVEAAPGTAQS 179
RC	STRAIN=GRI-90;	Do	130 KDEVKGKNNHCPVKAGHFONTSSPSARCOHPHRCEENDGIVLEAAMPQAQSRTC 183
RA	Shchelkunov S.N., Safronov P.F., Petrov N.A., Gutorov V.V., Kotwal G.J.,	Do	139 TDTV-----CHPCPVGFSSNQSLFEKCYPWTSCEDKNLLEVLOKGTSINVIC 186
RA	Riazankina O.I.,' Petrov N.A., Gutorov V.V., Miheev M.V.,	Do	148 --QRVQKGTESQDTLQNCPGTF-SSTNGTLEECOHNKCSKWLVEAGPOTISS 200
RA	Ryazankina O.I.,' Petrov N.A., Gutorov V.V., Miheev M.V.,	Do	91 SKCLOCQCMDPAMGLRTSRNSCTANALGCGCSPGHFCITQDGPHCAACRAYATSSPG-- 147
RA	Ryazankina O.I.,' Petrov N.A., Gutorov V.V., Miheev M.V.,	Do	128 ELKDEEVGGNNH---CVPKCAGHFONTSSPSARCOHTRCENQGLVEAAPGTAQS 179
RA	Ryazankina O.I.,' Petrov N.A., Gutorov V.V., Miheev M.V.,	Do	130 KDEVKGKNNHCPVKAGHFONTSSPSARCOHPHRCEENDGIVLEAAMPQAQSRTC 183
RT	"Structure-function and organization of cowpox virus strain GRI-90,"	Do	139 TDTV-----CHPCPVGFSSNQSLFEKCYPWTSCEDKNLLEVLOKGTSINVIC 186
RT	complete genome."	Do	148 --QRVQKGTESQDTLQNCPGTF-SSTNGTLEECOHNKCSKWLVEAGPOTISS 200
RL	Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.	Do	91 SKCLOCQCMDPAMGLRTSRNSCTANALGCGCSPGHFCITQDGPHCAACRAYATSSPG-- 147
RN	[4]	Do	128 ELKDEEVGGNNH---CVPKCAGHFONTSSPSARCOHTRCENQGLVEAAPGTAQS 179
RP	SEQUENCE FROM N.A.	Do	130 KDEVKGKNNHCPVKAGHFONTSSPSARCOHPHRCEENDGIVLEAAMPQAQSRTC 183
RC	STRAIN=GRI-90;	Do	139 TDTV-----CHPCPVGFSSNQSLFEKCYPWTSCEDKNLLEVLOKGTSINVIC 186
RA	Totmenin A. V.;	Do	148 --QRVQKGTESQDTLQNCPGTF-SSTNGTLEECOHNKCSKWLVEAGPOTISS 200
RL	Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.	Do	91 SKCLOCQCMDPAMGLRTSRNSCTANALGCGCSPGHFCITQDGPHCAACRAYATSSPG-- 147
DR	EMBL; X94355; CADD023.1; -.	Do	128 ELKDEEVGGNNH---CVPKCAGHFONTSSPSARCOHTRCENQGLVEAAPGTAQS 179
DR	HSSP; Q95961; JUNA.	Do	130 KDEVKGKNNHCPVKAGHFONTSSPSARCOHPHRCEENDGIVLEAAMPQAQSRTC 183
DR	GO; GO:0004872; F:receptor activity; IEA.	Do	139 TDTV-----CHPCPVGFSSNQSLFEKCYPWTSCEDKNLLEVLOKGTSINVIC 186
DR	InterPro; IPR001368; TNFR_c6.	Do	148 --QRVQKGTESQDTLQNCPGTF-SSTNGTLEECOHNKCSKWLVEAGPOTISS 200
DR	InterPro; IPR008063; Fas receptor.	Do	91 SKCLOCQCMDPAMGLRTSRNSCTANALGCGCSPGHFCITQDGPHCAACRAYATSSPG-- 147
DR	InterPro; IPR001368; TNFR_c6.	Do	128 ELKDEEVGGNNH---CVPKCAGHFONTSSPSARCOHTRCENQGLVEAAPGTAQS 179
DR	PF00020; TNFR_c6; 3.	Do	130 KDEVKGKNNHCPVKAGHFONTSSPSARCOHPHRCEENDGIVLEAAMPQAQSRTC 183
DR	PRINTS; PRO1680; FASRECEPTOR.	Do	139 TDTV-----CHPCPVGFSSNQSLFEKCYPWTSCEDKNLLEVLOKGTSINVIC 186
DR	SMART; SM00208; TNFR_3.	Do	148 --QRVQKGTESQDTLQNCPGTF-SSTNGTLEECOHNKCSKWLVEAGPOTISS 200
DR	PROSITE; PS00052; TNFR_NGFR_1; 1.	Do	91 SKCLOCQCMDPAMGLRTSRNSCTANALGCGCSPGHFCITQDGPHCAACRAYATSSPG-- 147
DR	PROSITE; PS55050; TNFR_NGFR_2; 2.	Do	128 ELKDEEVGGNNH---CVPKCAGHFONTSSPSARCOHTRCENQGLVEAAPGTAQS 179

Query Match 21.2%; Score 240; DB 12; Length 186;  
 Best Local Similarity 32.2%; Pred. No. 4e-18; Matches 48; Conservative 25; Mismatches 66; Indels 10; Gaps 5; Matches 48;

QY 3 PQAVPPYASENQTRDQEKEYYEPOHRICSRCPGTYSAKSIRIDTVCATGAENSY 62  
 Db 24 PTPUPPHAPVNGSC--DEGYLDKRNQCNQCPGEFKYRCSGSDWTKCERCPHIFT 81  
 QY 63 EHWNYLITQCRLCRCDPVMGLEBLAPCTSRRKTQCRQGMFCA---AWALECTHCELS 119  
 Db 82 ALPNISNGHQCRKC-PFGSFDKV-KCTGTNSKSCSCLPGWYCATDSSOTEDCRDCVPKS 139

QY 120 DCPPGTEALKDENGKGNHHCVCKAGHF 148  
 Db 140 RCPGCGYFGGIDEQ--GNPICKSCCVGVYE 165

---

RESULT 15

Q7T2H3 PRELIMINARY; PRT: 318 AA.

ID Q7T2H3  
 AC Q7T2H3;  
 DT 01-OCT-2003 (TREMBrel: 25, Created)  
 DT 01-OCT-2003 (TREMBrel: 25, Last sequence update)  
 DT 01-OCT-2003 (TREMBrel: 25, Last annotation update)

DB Tumour necrosis factor receptor.

GN INFR.

OS Oncorhynchus mykiss (Rainbow trout) (*Salmo gairdneri*)

OC Eukaryota; Metazoa; Chordata; vertebrata; Buteleostomi;

OC Actinopercygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopercygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI\_TaxID=8022;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Head kidney;

RA Zou J., Secombes C.J.;  
 RT "Molecular cloning and expression analysis of a TNF receptor homologue  
 RT in rainbow trout, *Oncorhynchus mykiss*";  
 RL Submitted (Nov-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AUS17804; CAD57165.1; -.

KW Receptor.

SEQUENCE 318 AA; 33254 MW; 78F81350112B3B43 CRC64;

SQ Query Match 21.1%; Score 238.5; DB 13; length 318;  
 Best Local Similarity 29.1%; Pred. No. 1e-17; Matches 50; Conservative 22; Mismatches 89; Indels 11; Gaps 3; Matches 50;

QY 15 CRDQEKEYEPOHRICSRCPGTYSAKSIRIDTVCATCAENSYNEHWNYLTICQLR 75  
 Db 6 CKTBEYLHDAASGVKRCCERKGQYVTRTGGSKTKTECHTCQHEYYTABILNFLKQCLR 65  
 QY 76 PCDPVMGLEBLAPCTSRRKTQCRQGMFCAAWALECTHCELSDCPPTSTEAEKLDEYVK 135  
 Db 65 VCYSSSNQKVLCRECAASSRQCVCKTGIVCTDDG--CETCIPVNLCPMSGV---VNQ 118

QY 136 GNHH---CYPCKAHRFQWPSSPSARCPPTRCENQGLYEAAPGTAQSMRTTC 183  
 Db 119 ANPQNDTVAPCQPGTINSFNDAFTHCQSHTRCGDLGKEVKSAGETTDVC 170

Search completed: August 28, 2004, 01:49:03  
 Job time : 119 secs

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GenCore version 5.1.6  
copyright (c) 1993 - 2004 Compugen Ltd.

### OM protein - protein search, using sw model

Run on:

August 28, 2004, 01:44:58 ; Search time 32 Seconds

Perfect score: 317.822 Million cell updates/sec

**Title:** US-10-003-211-1  
**Sequence:** 1 SQPQAVPPYASENOTCRDQE . . . . . QSDTICKNPLEPLPPEMSGT 197  
**Scoring table:** BLOSUM62  
**Gapop:** 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

**Database :** Issued Patents AA:\*

1: /cgn2\_6/podata/2/iaa/5A\_COMB.pep:\*

2: /cgn2\_6/podata/2/iaa/5B\_COMB.pep:\*

3: /cgn2\_6/podata/2/iaa/\_COMB.pep:\*

4: /cgn2\_6/podata/2/iaa/6B\_COMB.pep:\*

5: /cgn2\_6/podata/2/iaa/PCUTS\_COMB.pep:\*

6: /cgn2\_6/podata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description	
1	1133	100.0	197	2	US-08-505-606-1	
2	1133	100.0	197	4	US-09-000-166-1	
3	100.0	197	4	US-09-302-262-1	Sequence 1, Appli	
4	98.7	170	4	US-08-820-683A-14	Sequence 1, Appli	
5	98.1	86.6	170	4	US-09-523-323-57	Sequence 14, Appli
6	77.1	68.0	415	3	US-09-005-353A-6	Sequence 57, Appli
7	77.1	68.0	415	4	US-09-573-986-6	Sequence 6, Appli
8	45.6	40.2	77	3	US-08-865-545-3	Sequence 6, Appli
9	45.6	40.2	77	4	US-09-627-975-3	Sequence 3, Appli
10	30.5	26.9	227	3	US-08-974-022-48	Sequence 48, Appli
11	30.5	26.9	227	3	US-08-795-445A-48	Sequence 48, Appli
12	30.5	26.9	227	3	US-08-795-447A-48	Sequence 48, Appli
13	30.5	26.9	227	3	US-08-974-186-48	Sequence 48, Appli
14	30.5	26.9	227	3	US-08-795-446B-48	Sequence 48, Appli
15	30.5	26.9	227	4	US-08-706-945D-134	Sequence 134, Appli
16	30.5	26.9	227	4	US-08-577-788C-48	Sequence 48, Appli
17	30.5	26.9	235	4	US-09-326-394-48	Sequence 4, Appli
18	30.5	26.9	235	4	US-09-580-235-2	Sequence 2, Appli
19	30.5	26.9	235	4	US-09-580-235-8	Sequence 8, Appli
20	30.5	26.9	235	4	US-09-580-181-2	Sequence 2, Appli
21	30.5	26.9	235	4	US-09-580-181-8	Sequence 8, Appli
22	30.5	26.9	235	4	US-09-022-530-2	Sequence 2, Appli
23	30.5	26.9	235	4	US-09-102-531-8	Sequence 8, Appli
24	30.5	26.9	257	4	US-09-519-845-10	Sequence 10, Appli
25	30.5	26.9	461	2	US-08-385-229-2	Sequence 2, Appli
26	30.5	26.9	461	2	US-08-650-000-2	Sequence 2, Appli
27	30.5	26.9	461	3	US-09-042-783A-7	Sequence 7, Appli

**RESULT 1:  
US-08-505-606-1**

; Sequence 1, Application US/08505606  
; Patient No. 5925351  
; GENERAL INFORMATION:  
; APPLICANT: BROWNING, Jeffrey L.  
; APPLICANT: HOCHMAN, Paula S.  
; TIME OF INVENTION: SOLUBLE LYMPHOTOXIN-BETA RECEPTORS AND  
; TIME OF INVENTION: ANTI-LYMPHOTOXIN RECEPTOR AND LIGAND ANTIBODIES AS  
; TITLE OF INVENTION: THERAPEUTIC AGENTS FOR THE TREATMENT OF IMMUNOLOGICAL  
; TITLE OF INVENTION: DISEASE  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr.  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/505,606  
; FILING DATE: 21-JUL-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/378,968  
; FILING DATE: 26-JAN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HALEY, JR., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: B191  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 596-9900  
; TELEFAX: (212) 596-9900  
; TELEX: 14-8367  
; INFORMATION FOR SBO ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 197 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-505-606-1

Query Match 100.0%; Score 1133; DB 2; Length 197;

Best Local Similarity 100.0%; Pred. No. 2.5e-99; DISEASE

Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQPQAVPPYASENOTCRDQEKEYEPRHRICSRCPGTVYSAKCSRIRDTCATCAENS 60

Db 1 SQPQAVPPYASENOTCRDQEKEYEPRHRICSRCPGTVYSAKCSRIRDTCATCAENS 60

QY 61 YNEHWNLYTICOLCRCPDPVMGLEETAPCTSRSKRKTOCRCPGMFCAAWALECTHCELLSD 120

Db 61 YNEHWNLYTICOLCRCPDPVMGLEETAPCTSRSKRKTOCRCPGMFCAAWALECTHCELLSD 120

QY 181 TTCKNPLEPLPPEMSGT 197

Db 181 TTCKNPLEPLPPEMSGT 197

RESULT 2

US-09-000-166-1

; Sequence 1, Application US/09000166A

; Patent No. 6403087

; GENERAL INFORMATION:

; APPLICANT: Browning, et al.

; TITLE OF INVENTION: Soluble Lymphotoxin-B Receptors and Anti-Lymphotoxin

; INVENTION: Receptor and Ligand Antibodies, as Therapeutic Agents

; TITLE OF INVENTION: For the Treatment of Immunological Disease.

; FILE REFERENCE: B191

; CURRENT APPLICATION NUMBER: US/09/000,166A

; CURRENT FILING DATE: 1998-06-08

; EARLIER APPLICATION NUMBER: PCT/US96/12010

; EARLIER FILING DATE: 1996-07-19

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 197

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-000-166-1

Query Match 100.0%; Score 1133; DB 4; Length 197;

Best Local Similarity 100.0%; Pred. No. 2.5e-99; DISEASE

Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQPQAVPPYASENOTCRDQEKEYEPRHRICSRCPGTVYSAKCSRIRDTCATCAENS 60

Db 1 SQPQAVPPYASENOTCRDQEKEYEPRHRICSRCPGTVYSAKCSRIRDTCATCAENS 60

QY 61 YNEHWNLYTICOLCRCPDPVMGLEETAPCTSRSKRKTOCRCPGMFCAAWALECTHCELLSD 120

Db 61 YNEHWNLYTICOLCRCPDPVMGLEETAPCTSRSKRKTOCRCPGMFCAAWALECTHCELLSD 120

QY 121 CPPGTEAELKDEVGKGNNHCVPCKAGHFONTSSPSPARCQPHTRCENQGLIVEAAPGTAQSD 180

Db 121 CPPGTEAELKDEVGKGNNHCVPCKAGHFONTSSPSPARCQPHTRCENQGLIVEAAPGTAQSD 180

QY 181 TTCKNPLEPLPPEMSGT 197

Db 181 TTCKNPLEPLPPEMSGT 197

RESULT 3

US-09-303-262-1

; Sequence 1, Application US/09303262

; Patent No. 6569941

; GENERAL INFORMATION:

; APPLICANT: Browning, Jeffrey L.

; BENJAMIN, Christopher D.

; HOCHMAN, Paula S.

; TITLE OF INVENTION: SOLUBLE LYMPHOTOXIN-BETA RECEPTORS AND

; ANTI-LYMPHOTOXIN RECEPTOR AND LIGAND ANTIBODIES AS

THERAPEUTIC AGENTS FOR THE TREATMENT OF IMMUNOLOGICAL DISEASE

NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr.

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10020

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/303,262

FILING DATE: 30-Apr-1999

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/505,606

FILING DATE: 21-JUL-1995

APPLICATION NUMBER: US 08/378,968

FILING DATE: 26-JAN-1995

ATTORNEY/AGENT INFORMATION:

NAME: HALEY, JR., James F.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: B191

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 596-9090

TELEX: 14-8367

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 197 amino acids

TYPE: amino acid

STRANDEDNESS: &lt;Unknown&gt;

TOPOLOGY: linear

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-303-262-1

Query Match 100.0%; Score 1133; DB 4; Length 197;

Best Local Similarity 100.0%; Pred. No. 2.5e-99; DISEASE

Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQPQAVPPYASENOTCRDQEKEYEPRHRICSRCPGTVYSAKCSRIRDTCATCAENS 60

Db 1 SQPQAVPPYASENOTCRDQEKEYEPRHRICSRCPGTVYSAKCSRIRDTCATCAENS 60

QY 61 YNEHWNLYTICOLCRCPDPVMGLEETAPCTSRSKRKTOCRCPGMFCAAWALECTHCELLSD 120

Db 61 YNEHWNLYTICOLCRCPDPVMGLEETAPCTSRSKRKTOCRCPGMFCAAWALECTHCELLSD 120

QY 121 CPPGTEAELKDEVGKGNNHCVPCKAGHFONTPSSPSPARCQPHTRCENQGLIVEAAPGTAQSD 180

Db 121 CPPGTEAELKDEVGKGNNHCVPCKAGHFONTPSSPSPARCQPHTRCENQGLIVEAAPGTAQSD 180

QY 181 TTCKNPLEPLPPEMSGT 197

Db 181 TTCKNPLEPLPPEMSGT 197

RESULT 4

US-08-828-683A-14

; Sequence 14, Application US/08828683A

; Patent No. 6469144

; GENERAL INFORMATION:

; APPLICANT: Askenazi, Avi J

; TITLE OF INVENTION: Apo-2 Li AND Apo-3 POLYPEPTIDES

; NUMBER OF SEQ ID NOS: 28

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/828,683A  
 FILING DATE: 31-Mar-1997  
 CLASSIFICATION: <Unknown>  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/625328  
 FILING DATE: 1-Apr-1996  
 APPLICATION NUMBER: 08/710802  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Marschang, Diane L.  
 REFERENCE/DOCKET NUMBER: 35,600  
 REGISTRATION NUMBER: 08/710801  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650/225-5416  
 TELEFAX: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 170 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
 ; US-08-828-683A-14

Query Match 87.1%; Score 987; DB 4; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-85;  
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TCDQDKKEYPQRHICCSRPPGTVWSAKSRSRDTVCACTAENSYNEHHNLYTICQLC 74  
 Db 1 TCDQDKKEYPQRHICCSRPPGTVWSAKSRSRDTVCACTAENSYNEHHNLYTICQLC 60

Qy 75 RCPDPYNGLEETAPCTSKRKTKQRCOPGMFCAWALEBCTHCELLSDCPPGTEAEKLDEVG 134  
 Db 61 RCPDPYNGLEETAPCTSKRKTKQRCOPGMFCAWALEBCTHCELLSDCPPGTEAEKLDEVG 120

Qy 135 KGNNHCVCKAGHFONTSSPSARCQPHTRCENQGLVEAARGTAQSITCK 184  
 Db 121 KGNNHCVCKAGHFONTSSPSARCQPHTRCENQGLVEAARGTAQSITCK 170

RESULT 5  
 US-09-523-323-57  
 ; Sequence 57, Application US/09523323

GENERAL INFORMATION:  
 ; APPLICANT: Ebner, Reinhard  
 ; APPLICANT: Yu, Guo-Liang  
 ; APPLICANT: Ruben, Steven M.  
 ; APPLICANT: Ulrich, Stephen  
 ; APPLICANT: Zhai, Yifan  
 TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use  
 FILE REFERENCE: 1488.065000C  
 CURRENT APPLICATION NUMBER: US/09/523,323  
 CURRENT FILING DATE: 2000-03-10  
 EARLIER APPLICATION NUMBER: 60/168,380  
 EARLIER FILING DATE: 1999-12-02  
 EARLIER APPLICATION NUMBER: 60/148,326  
 EARLIER FILING DATE: 1999-08-11  
 EARLIER APPLICATION NUMBER: 60/142,657  
 EARLIER FILING DATE: 1999-07-06  
 EARLIER APPLICATION NUMBER: 60/137,457  
 EARLIER FILING DATE: 1999-06-04

RESULT 5  
 US-09-523-323-57  
 ; Sequence 57, Application US/09523323

GENERAL INFORMATION:  
 ; APPLICANT: Ebner, Reinhard  
 ; APPLICANT: Yu, Guo-Liang  
 ; APPLICANT: Ruben, Steven M.  
 ; APPLICANT: Ulrich, Stephen  
 ; APPLICANT: Zhai, Yifan  
 TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use  
 FILE REFERENCE: 1488.065000C  
 CURRENT APPLICATION NUMBER: US/09/523,323  
 CURRENT FILING DATE: 2000-03-10  
 EARLIER APPLICATION NUMBER: 60/168,380  
 EARLIER FILING DATE: 1999-12-02  
 EARLIER APPLICATION NUMBER: 60/148,326  
 EARLIER FILING DATE: 1999-08-11  
 EARLIER APPLICATION NUMBER: 60/142,657  
 EARLIER FILING DATE: 1999-07-06  
 EARLIER APPLICATION NUMBER: 60/137,457  
 EARLIER FILING DATE: 1999-06-04

RESULT 6  
 US-09-006-353A-6  
 ; Sequence 6, Application US/09006353A

GENERAL INFORMATION:  
 ; APPLICANT: WEI, YING-FEI  
 ; APPLICANT: YU, GUO-LIANG  
 ; APPLICANT: GENZI, REINER  
 ; APPLICANT: RUBEN, STEVEN  
 TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5  
 NUMBER OF SEQUENCES: 26  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
 STREET: 9410 WEST AVENUE  
 CITY: ROCKVILLE  
 STATE: MD  
 COUNTRY: US  
 ZIP: 20850

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/006,353A  
 FILING DATE:  
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: BROOKES, ANDERS A  
 REGISTRATION NUMBER: 36,373  
 REFERENCE/DOCKET NUMBER: PP341  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (301) 309-8504  
 TELEFAX: (301) 309-8512  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 415 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLogy: linear  
 MOLECULE TYPE: protein  
 US-09-006-353A-6

Query Match 68.0%; Score 771; DB 3; Length 415;  
 Best Local Similarity 70.7%; Pred No. 7.1e-65; Mismatches 14; Indels 40; Gaps 1;  
 Matches 135; Conservative

QY 1 SQOPAQVPPYASENOTCRDQEKEYEPRHICCSRCPGTVYSAKCSRIRDTCATAENS 60  
 Db 28 SQQPOLVPYRITENQTCWDQDKEYEFPMHDVCCSRCPGFERFAVRSRQDTVKCIPHS 87

QY 61 YNEHHWNLITICOLCRCPGMELAPCTSKRKTKOCRCQPMFCAAWALE 118  
 Db 88 YNEHHWNLSTCQCRCRDPDVGFERFAVPTCSDRKAECRCQPMGCVYLNECHICBEERL 147

QY 119 SDCPPGTEAKLKDREVKGKNNHCVPCKAGHRNTSPSARCCQHTRCENQIVLEAPGTAQ 178  
 Db 148 VLGQPTEAEVDEIMDIDVNCVPCKPGRHQTSSPRACQPHRCIQLQVVEARGTSY 207

QY 179 SDTICKNPLEP 189  
 Db 208 SDTICKNPEP 218

RESULT 7  
 US-09-573-986-6  
 ; Sequence 6, Application US/09573986  
 ; Patent No. 6455040  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wei, Ying-Fei  
 ; APPLICANT: Ni, Jian  
 ; APPLICANT: Genth, Reiner  
 ; APPLICANT: Ruben, Steven  
 ; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5  
 ; FILE REFERENCE: 1488-1280004  
 ; CURRENT APPLICATION NUMBER: US/09/573,986  
 ; CURRENT FILING DATE: 2000-05-18  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 6  
 ; LENGTH: 415  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-573-986-6

Query Match 68.0%; Score 771; DB 4; Length 415;  
 Best Local Similarity 70.7%; Pred No. 7.1e-65; Mismatches 14; Indels 40; Gaps 1;  
 Matches 135; Conservative 14; Mismatches 40; Indels 2; Gaps 1;

QY 1 SQOPAQVPPYASENOTCRDQEKEYEPRHICCSRCPGTVYSAKCSRIRDTCATAENS 60  
 Db 28 SQQPOLVPYRITENQTCWDQDKEYEFPMHDVCCSRCPGFERFAVRSRQDTVKCIPHS 87

QY 61 YNEHHWNLITICOLCRCPGMELAPCTSKRKTKOCRCQPMFCAAWALE 118  
 Db 88 YNEHHWNLSTCQCRCRDPDVGFERFAVPTCSDRKAECRCQPMGCVYLNECHICBEERL 147

RESULT 8  
 US-08-866-545-3  
 ; Sequence 3, Application US/08866545  
 ; Patent No. 626535  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Greene, Mark I.  
 ; APPLICANT: Murali, Ramachandran  
 ; APPLICANT: Takasaki, Wataru  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pennie & Edmonds LLP  
 ; STREET: 115 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: NY  
 ; COUNTRY: USA  
 ; ZIP: 10036-2811  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSEQ Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/866,545  
 ; FILING DATE: 30-MAY-1997  
 ; CLASSIFICATION: 530  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Coruzzi, Laura A  
 ; REGISTRATION NUMBER: 30,742  
 ; REFERENCE/DOCKET NUMBER: 009113-004-999  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650-493-4935  
 ; TELEFAX: 650-493-5556  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 77 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLogy: linear  
 ; MOLECULE TYPE: No. 6265535e  
 ; US-08-866-545-3

Query Match 40.2%; Score 456; DB 3; Length 77;  
 Best Local Similarity 40.0%; Pred No. 5.1e-36; Mismatches 0; Indels 0; Gaps 0;  
 Matches 77; Conservative

QY 52 VCATCAENSYNEHHWNLITICOLCRCPGMELAPCTSKRKTKOCRCQPMFCAAWALE 111  
 Db 1 VCATCAENSYNEHHWNLITICOLCRCPGMELAPCTSKRKTKOCRCQPMFCAAWALE 60

QY 112 CTCHCELLSDCIPGTEA 128  
 Db 61 CTCHCELLSDCIPGTEA 77

RESULT 9  
 US-09-627-775-3  
 ; Sequence 3, Application US/09627775  
 ; Patent No. 6682739  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Greene, Mark

APPLICANT: Murali, Ramachandran  
 APPLICANT: Aoki, Kazuhiko  
 APPLICANT: Balon, Roland  
 TITLE OF INVENTION: Methods of Inhibiting Osteoclastogenesis  
 CURRENT APPLICATION NUMBER: US/09/627,775  
 CURRENT FILING DATE: 2000-07-28  
 PRIORITY APPLICATION NUMBER: 60/146,090  
 PRIORITY FILING DATE: 1999-07-28  
 NUMBER OF SEQ ID NOS: 29  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 3  
 LENGTH: 77  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-627-775-3

Query Match 40.2%; Score 456; DB 4; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-36;  
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 AVPPWASE-NOTCROEKEYEPORRICKCSRCPPTSYVSAKCSRRTDTCATCAENSYNE 63  
 Db 28 AFTPAPAPEGSTCR--PCDPWGLEHTAPCTSKRKTOCRCOPGMFAAWALR-CTICELLS 119  
 QY 64 HNYLTICQLCR--PCDPWGLEHTAPCTSKRKTOCRCOPGMFAAWALR-CTICELLS 85  
 Db 86 LWNWVPECLSGSRSSDQV---EQACTREQNRLCTCRGFWYCALSKOBGCRICAPIR 141  
 QY 120 DCPPG-----TEAK-KDEVKGNNICVPCAGHONTSSSARCPBHTRENQIYEAAP 174  
 Db 142 KCRPGRGVARPGETSDVV-----CKPCAPGTSNTSSDICHPHQICN---VVAIP 191  
 QY 175 GTAQSDTC--KNPPEPLPP 192  
 Db 192 GNASIDAVCTSTSPPRSMAP 211

RESULT 10

US-08-974-022-48

Sequence 48 Application US/08974022  
 Patient No. 6015938  
 GENERAL INFORMATION:  
 APPLICANT: Boyle, William J.  
 APPLICANT: Lacey, David L.  
 APPLICANT: Chang, Ming-Shi  
 TITLE OF INVENTION: OSTEOPROTEGERIN  
 NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Amgen Inc.  
 STREET: 1840 Dehavenilland Drive  
 CITY: Thousand Oaks  
 STATE: California  
 COUNTRY: USA  
 ZIP: 91320-1789

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/974,022  
 FILING DATE: 12-DEC-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/577,788

FILING DATE:

ATTORNEY/AGENT INFORMATION:  
 NAME: Winter, Robert B.  
 REFERENCE/DOCKET NUMBER: A-378

INFORMATION FOR SEQ ID NO: 48:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 227 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-795-445A-48

Query Match 26.9%; Score 305; DB 3; Length 227;  
 Best Local Similarity 35.0%; Pred. No. 2.8e-21;  
 Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;

Query Match

26.9%; Score 305; DB 3; Length 227;

Best Local Similarity 35.0%; Pred. No. 2.8e-21;  
 Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;  
 QY 5 AVPPWASE-NOTCROEKEYEPORRICKCSRCPPTSYVSAKCSRRTDTCATCAENSYNE 63  
 Db 28 AFTPAPAPEGSTCR--PCDPWGLEHTAPCTSKRKTOCRCOPGMFAAWALR-CTICELLS 119  
 QY 64 HNYLTICQLCR--PCDPWGLEHTAPCTSKRKTOCRCOPGMFAAWALR-CTICELLS 85  
 Db 86 LWNWVPECLSGSRSSDQV---EQACTREQNRLCTCRGFWYCALSKOBGCRICAPIR 141  
 QY 120 DCPPG-----TEAK-KDEVKGNNICVPCAGHONTSSSARCPBHTRENQIYEAAP 174  
 Db 142 KCRPGRGVARPGETSDVV-----CKPCAPGTSNTSSDICHPHQICN---VVAIP 191  
 QY 175 GTAQSDTC--KNPPEPLPP 192  
 Db 192 GNASIDAVCTSTSPPRSMAP 211

RESULT 11

US-08-795-445A-48

Sequence 48 Application US/0897445A  
 Patient No. 6284485

GENERAL INFORMATION:

APPLICANT: Boyle, William J.  
 APPLICANT: Lacey, David L.  
 APPLICANT: Calzone, Frank J.  
 APPLICANT: Chang, Ming-Shi

TITLE OF INVENTION: OSTEOPROTEGERIN

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Inc.  
 STREET: 1840 Dehavenilland Drive  
 CITY: Thousand Oaks  
 STATE: California  
 COUNTRY: USA  
 ZIP: 91320-1789

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/795,445A

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/577,788

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Winter, Robert B.  
 REFERENCE/DOCKET NUMBER: A-378

INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 227 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-08-795-445A-48

Query Match 26.9%; Score 305; DB 3; Length 227;  
 Best Local Similarity 35.0%; Pred. No. 2.8e-21;  
 Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;

QY 5 AVPPWASE-NOTCROEKEYEPORRICKCSRCPPTSYVSAKCSRRTDTCATCAENSYNE 63  
 Db 28 AFTPAPAPEGSTCR--PCDPWGLEHTAPCTSKRKTOCRCOPGMFAAWALR-CTICELLS 119  
 QY 64 HNYLTICQLCR--PCDPWGLEHTAPCTSKRKTOCRCOPGMFAAWALR-CTICELLS 85  
 Db 86 LWNWVPECLSGSRSSDQV---EQACTREQNRLCTCRGFWYCALSKOBGCRICAPIR 141  
 QY 120 DCPPG-----TEAK-KDEVKGNNICVPCAGHONTSSSARCPBHTRENQIYEAAP 174  
 Db 142 KCRPGRGVARPGETSDVV-----CKPCAPGTSNTSSDICHPHQICN---VVAIP 191  
 QY 175 GTAQSDTC--KNPPEPLPP 192  
 Db 192 GNASIDAVCTSTSPPRSMAP 211

RESULT 12  
US-08-795-447A-48  
; Sequence 48, Application US/08795447A  
; Patent No. 6284728  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: OSTROPROTEGERIN  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Angen Inc.  
; STREET: One Angen Center Drive  
; CITY: Thousand Oaks  
; STATE: California  
; ZIP: 91340-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,186  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378D2  
; INFORMATION FOR SEQ ID NO: 48:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 227 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: Single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-795-447A-48  
; Query Match 26.9%; Score 305; DB 3; Length 227;  
; Best Local Similarity 35.0%; Pred. No. 2.8e-21;  
; Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;  
; Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;  
; QY 5 AVPVAYASE NOTCRODEKEKYEPPQRHICCSRCPGTYNSAKCSRIRDTCATCAENSYNE 63  
; DB 28 AFTPYAPPEPGSTCR-LREYYDQTAQMCCSKCSPGQHAKVFCIKTSDTVCDSCDSTYIQ 85  
; QY 64 HWNLYITIQCQLR--PDCPVMGLHIAPTTSKRKIQRCOPGMTCAAWALE-CTHCELLS 119  
; DB 86 LWNWVPECLSGSRCSQDV--EFOACTREONRICTCERGWYCALSKOEGCRLLCAPLR 141  
; QY 120 DCPPG----TEAELKDEVKGNNHCVPCKAGHFONTSSPARCOPHTRCENQGLVEAAP 174  
; DB 142 KCRPGFGVARPGTETSDVV----CKPCAPGTFSNTSSDICRPHQICN---VVAIP 191  
; QY 175 GQAQSDFTC-KNPLPPLPP 192  
; DB 192 GNASRDAVCTSTSPTRSMAP 211  
; RESULT 13  
US-08-974-186-48  
; Sequence 48, Application US/08974186  
; ; Sequence 48, Application US/08795446B  
; ; Patent No. 6288032  
; ; GENERAL INFORMATION:  
; ; APPLICANT: Boyle, William J.  
; ; APPLICANT: Lacey, David L.  
; ; APPLICANT: Calzone, Frank J.  
; ; APPLICANT: Chang, Ming-Shi  
; ; TITLE OF INVENTION: OSTROPROTEGERIN  
; ; NUMBER OF SEQUENCES: 53  
; ; CORRESPONDENCE ADDRESS:  
; ; ADDRESSEE: Angen Inc.

STREET: 1840 Dehavenland Drive  
 CITY: Thousand Oaks  
 STATE: California  
 COUNTRY: USA  
 ZIP: 91320-1789

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/795,446B  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/577,788  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 227 amino acids  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-795-446B-48

Query Match 26.9%; Score 305; DB 3; Length 227;  
 Best Local Similarity 35.0%; Pred. No. 2.8e-21; Indels 28; Gaps 9;  
 Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;

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Db      28 AFTPYAPEGSTCR--LRBEYDYDTAQMCSSKCSPGQHAKVFCTKTSDFCDSDTQ 85
QY      64 HWNLYTICOLCR--PCDPVNGLEETAPCTSKRKHQCRQCPGMFCAAWALE-CTHCELLS 119
Db      86 LWNWVPECLSGSRSDDQV---ETQACTREQRNRCITCRPGWVCAALSQEGCRLCAPR 141
QY      120 DCPPG----TEAELKDEVGKNNHCVPKAGHNTSPSARCPHTRCENQGLVEAAP 174
Db      142 KCRPGFGVARPGTETSDVV----CKPCAPGTFNTSSTDICRPHQCN---VVATP 191
QY      175 GIAQSSTTC--KNPLERLPP 192
Db      192 GNASRDAVCTSTSPTSMAP 211

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 Job time : 33 secs

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RESULT 15  
 US-08-706-945D-134  
 Sequence 134, Application US/0806945D  
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 GENERAL INFORMATION:  
 ; Paten t No. 6369027  
 ; APPLICANT: Boyle, William  
 ; APPLICANT: Lacey, David  
 ; APPLICANT: Calzone, Frank  
 ; APPLICANT: Chang, Ming-Shi  
 ; TITLE OF INVENTION: Osteoprotectorin  
 ; FILE REFERENCE: A-378CIP  
 ; CURRENT APPLICATION NUMBER: US/08/706, 945D  
 ; CURRENT FILING DATE: 1996-09-03  
 ; PRIORITY APPLICATION NUMBER: 08/577,788  
 ; PRIORITY FILING DATE: 1995-12-22  
 ; NUMBER OF SEQ ID NOS: 145  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO: 134  
 ; LENGTH: 227  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-08-706-945D-134

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## OM protein - protein search, using sw model

Run on:

August 28, 2004, 01:47:13 ; Search time 125 Seconds

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495.830 Million cell updates/sec

## Title:

US-10-003-211-1

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## Sequence:

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## Scoring table:

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Gapop 10.0 , Gapext 0.5

## Searched:

1297172 seqs, 314612898 residues

## Total number of hits satisfying chosen parameters:

1297172

## Minimum DB seq length:

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## Maximum DB seq length:

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## Post-processing:

Minimum Match 0%

Maximum Match 100%

listing first 45 summaries

## Database :

Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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2	1133	100.0	435	9 US-09-907-372-19
3	1133	100.0	435	9 US-09-917-372-19
4	1133	100.0	435	10 US-09-917-372-19
5	1133	100.0	435	12 US-10-087-192-942
6	1133	100.0	435	14 US-10-293-480-6
7	1133	100.0	435	15 US-10-365-300-17
8	1133	100.0	435	15 US-10-282-445-133
9	1129	99.6	399	9 US-09-907-372-1
10	1129	99.6	399	10 US-09-917-372-1
11	987	87.1	170	13 US-10-112-793-14
12	85.6	172	15	15 US-10-315-680-57
13	78.0	68.8	257	9 US-09-948-18-19
14	77.1	68.0	402	12 US-10-087-192-939
15	68.0	415	9 US-09-826-212-6	

## ALIGNMENTS

RESULT 1  
 US-10-003-211-1  
 ; Sequence 1, Application US/10003211  
 ; Publication No. US20020197254A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Biogen, Inc.  
 ; APPLICANT: Browning, et al.  
 ; TITLE OF INVENTION: Soluble Lymphotoxin Beta Receptor and Anti-Lymphotxin Receptor and Ligand Antibodies as Therapeutic Agents for the Treatment of Immunological Diseases  
 ; TITLE OF INVENTION: Therapeutic Agents for the Treatment of Immunological Diseases  
 FILE REFERENCE: A013US  
 CURRENT APPLICATION NUMBER: US/10/003,211  
 CURRENT FILING DATE: 2001-10-31  
 PRIOR APPLICATION NUMBER: PCT/US97/19436  
 PRIOR FILING DATE: 1997-10-24  
 PRIOR APPLICATION NUMBER: 60/029,060  
 PRIOR FILING DATE: 1996-10-25  
 NUMBER OF SEQ ID NOS: 1  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 1  
 LENGTH: 197  
 TYPE: PRT  
 ORGANISM: Homo Sapien  
 US-10-003-211-1  
 Query Match Best Local Similarity 100.0%; Score 1133; DB 13; Length 197;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 1 SQPQAVPPYASENQTCRDQEKEYEPQRHICRCRCPGTYVSAKCSRIRDVATCAENS 60  
 QY 61 YNEHWNYLTICOLCRPCDPVMGLFEEARCTSKRKTCRQSGMFAAWELECTHEELSD 120  
 Db 61 YNEHWNYLTICOLCRPCDPVMGLFEEARCTSKRKTCRQSGMFAAWELECTHEELSD 120

QY 121 CPPGTEAELKDEVKGKNNHCVPCKAGHFRONTSSPSARCOPHTRCENOLIVEAAGPTAQSD 180  
Db 121 CPPGTEAELKDEVKGKNNHCVPCKAGHFRONTSSPSARCOPHTRCENOLIVEAAGPTAQSD 180

QY 181 TTCKNPLEPLPPEMSGT 197  
Db 181 TTCKNPLEPLPPEMSGT 197

RESULT 2

US-09-907-372-19  
Sequence 19, Application US/09907372  
Patent No. US20020068242A1

GENERAL INFORMATION:

APPLICANT: Lal, Preeti G.

ATTORNEY/AGENT INFORMATION:  
NAME: KEENEY K. HOOVER

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/086, 582  
FILING DATE: <Unknown>

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/768, 779A  
FILING DATE: 25-Jan-2001  
CLASSIFICATION: <Unknown>

SEQUENCE CHARACTERISTICS:  
SEQUENCE: SEQ ID NO: 6:  
TYPE: amino acid  
STRANDEDNESS: single  
LENGTH: 435 amino acids  
TOPOLOGY: linear

MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-768-779A-6

Query Match 100.0%; Score 1133; DB 9; Length 435;  
Best Local Similarity 100.0%; Pred. No. 1.7e-88; Mismatches 0; Indels 0; Gaps 0;

Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OTHER INFORMATION: Incyte ID No. US20020068242A1 9339762

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Db 28 SQPQAQVPPYASENOTCRDQEKEYEYEPORHICCSRCPPGTIVSAKCSRIRDTCATCAENS 87

QY 61 YNEHWNLYTICQLCRPCDPVMGLBETAPCTSKRKTQCRQCPGMFCAAWALECTHELSD 120  
Db 88 YNEHWNLYTICQLCRPCDPVMGLBETAPCTSKRKTQCRQCPGMFCAAWALECTHELSD 147

QY 121 CPPGTEAELKDEVKGKNNHCVPCKAGHFRONTSSPSARCOPHTRCENOLIVEAAGPTAQSD 180  
Db 148 CPPGTEAELKDEVKGKNNHCVPCKAGHFRONTSSPSARCOPHTRCENOLIVEAAGPTAQSD 207

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Db 208 TTCKNPLEPLPPEMSGT 224

RESULT 4

US-09-917-372-19  
Sequence 19, Application US/09917372  
Publication No. US20030068619A1

GENERAL INFORMATION:  
APPLICANT: Lal, Preeti G.

ATTORNEY/AGENT INFORMATION:  
NAME: KEENEY K. HOOVER

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/086, 582  
FILING DATE: <Unknown>

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/917, 372  
FILING DATE: 2002-09-09

CLASSIFICATION: <Unknown>

SEQUENCE CHARACTERISTICS:  
SEQUENCE: SEQ ID NO: 6:  
TYPE: amino acid  
STRANDEDNESS: single  
LENGTH: 435 amino acids  
TOPOLOGY: linear

MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-917-372-19

Query Match 100.0%; Score 1133; DB 10; Length 435;  
Best Local Similarity 100.0%; Pred. No. 1.7e-88; Mismatches 0; Indels 0; Gaps 0;

Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OTHER INFORMATION: Incyte ID No. US20030068619A1 9339762

QY 1 SQPQAQVPPYASENOTCRDQEKEYEYEPORHICCSRCPPGTIVSAKCSRIRDTCATCAENS 60

RESULT 3

US-09-768-779A-6  
Sequence 6, Application US/0990779A  
Patent No. US2002012767A1

GENERAL INFORMATION:

APPLICANT: Lal, Preeti G.

ATTORNEY/AGENT INFORMATION:

NAME: KEENEY K. HOOVER

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/086, 582  
FILING DATE: <Unknown>

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/907, 372  
FILING DATE: 2001-07-27

CLASSIFICATION: <Unknown>

SEQUENCE CHARACTERISTICS:  
SEQUENCE: SEQ ID NO: 6:  
TYPE: amino acid  
STRANDEDNESS: single  
LENGTH: 435 amino acids  
TOPOLOGY: linear

MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-907-372-19

Query Match 100.0%; Score 1133; DB 9; Length 435;  
Best Local Similarity 100.0%; Pred. No. 1.7e-88; Mismatches 0; Indels 0; Gaps 0;

Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OTHER INFORMATION: Incyte ID No. US20020068242A1 9339762

Db 28 SQPQAVPPYASENQTCRDQEKEYEPOHRICCSRCPGTVSAKCSRIRDTCATCAENS 87  
 Qy 61 YNEHWNYLTICOLCRCPDPVNGLEIAPCTSKRKTOQCRCPGMFCAAWALECTBCELLSD 120  
 Db 88 YNEHWNYLTICOLCRCPDPVNGLEIAPCTSKRKTOQCRCPGMFCAAWALECTBCELLSD 147  
 ;  
 RESULT 5  
 US-10-087-192-942  
 ; Sequence 942, Application US/10087192  
 ; Publication No. US20020182586A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Morris, David W.  
 ; INVENTOR: Engelhard, Eric K.  
 ; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR  
 ; FILE REFERENCE: 52945200122  
 ; CURRENT APPLICATION NUMBER: US/10/087,192  
 ; CURRENT FILING DATE: 2002-03-01  
 ; PRIOR APPLICATION NUMBER: US 09/747,377  
 ; PRIOR FILING DATE: 2000-12-22  
 ; PRIOR APPLICATION NUMBER: US 09/798,586  
 ; PRIOR FILING DATE: 2001-03-02  
 ; NUMBER OF SEQ ID NOS: 2059  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 942  
 ; LENGTH: 435  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-087-192-942

Query Match 100.0%; Score 1133; DB 14; Length 435;  
 Best Local Similarity 100.0%; Pred. No. 1.-7e-88; 0; Mismatches 0; Indels 0; Gaps 0;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQPQAVPPYASENQTCRDQEKEYEPOHRICCSRCPGTVSAKCSRIRDTCATCAENS 60  
 Db 28 SQPQAVPPYASENQTCRDQEKEYEPOHRICCSRCPGTVSAKCSRIRDTCATCAENS 87  
 ;  
 Db 61 YNEHWNYLTICOLCRCPDPVNGLEIAPCTSKRKTOQCRCPGMFCAAWALECTBCELLSD 120  
 Qy 88 YNEHWNYLTICOLCRCPDPVNGLEIAPCTSKRKTOQCRCPGMFCAAWALECTBCELLSD 147  
 ;  
 RESULT 7  
 US-10-369-300-17  
 ; Sequence 17, Application US/10369300  
 ; Publication No. US2003021542A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Frasor, Christopher  
 ; INVENTOR: Hancock, Wayne  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OR PREVENTION OF  
 ; TITLE OF INVENTION: DISORDERS USING COMBINATION THERAPY  
 ; FILE REFERENCE: 7853-255  
 ; CURRENT APPLICATION NUMBER: US/10/369,300  
 ; CURRENT FILING DATE: 2003-02-19  
 ; PRIOR APPLICATION NUMBER: 60/358,463  
 ; PRIOR FILING DATE: 2002-02-19  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO: 17  
 ; LENGTH: 435  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-369-300-17

Query Match 100.0%; Score 1133; DB 15; Length 435;  
 Best Local Similarity 100.0%; Pred. No. 1.-7e-88; 0; Mismatches 0; Indels 0; Gaps 0;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQPQAVPPYASENQTCRDQEKEYEPOHRICCSRCPGTVSAKCSRIRDTCATCAENS 60  
 Db 28 SQPQAVPPYASENQTCRDQEKEYEPOHRICCSRCPGTVSAKCSRIRDTCATCAENS 87  
 ;  
 Db 61 YNEHWNYLTICOLCRCPDPVNGLEIAPCTSKRKTOQCRCPGMFCAAWALECTBCELLSD 120  
 Qy 88 YNEHWNYLTICOLCRCPDPVNGLEIAPCTSKRKTOQCRCPGMFCAAWALECTBCELLSD 147  
 ;  
 RESULT 6  
 US-10-291-480-6  
 ; Sequence 6, Application US/10291480  
 ; Publication No. US2003010069A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ni, Jian  
 ; APPLICANT: Moore, Paul  
 ; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Protein 8  
 ; FILE REFERENCE: PP368C1D1  
 ; CURRENT APPLICATION NUMBER: US/10/291,480  
 ; CURRENT FILING DATE: 2002-11-12  
 ; PRIOR APPLICATION NUMBER: 09/768,779

Db 121 CPPGTAEELKDEVGKGNNHCUPCKAGHFONTSSPARCQPHTRCENQGLVEAAPTAQSD 180  
 Qy 148 CPPGTAEELKDEVGKGNNHCUPCKAGHFONTSSPARCQPHTRCENQGLVEAAPTAQSD 207  
 ;  
 Db 208 TTCKNPLEPLPEMSGT 224  
 ;  
 ;  
 Query Match 100.0%; Score 1133; DB 14; Length 435;  
 Best Local Similarity 100.0%; Pred. No. 1.-7e-88; 0; Mismatches 0; Indels 0; Gaps 0;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQPQAVPPYASENQTCRDQEKEYEPOHRICCSRCPGTVSAKCSRIRDTCATCAENS 60  
 Db 28 SQPQAVPPYASENQTCRDQEKEYEPOHRICCSRCPGTVSAKCSRIRDTCATCAENS 87  
 ;  
 Db 61 YNEHWNYLTICOLCRCPDPVNGLEIAPCTSKRKTOQCRCPGMFCAAWALECTBCELLSD 120  
 Qy 88 YNEHWNYLTICOLCRCPDPVNGLEIAPCTSKRKTOQCRCPGMFCAAWALECTBCELLSD 147  
 ;  
 Db 121 CPPGTAEELKDEVGKGNNHCUPCKAGHFONTSSPARCQPHTRCENQGLVEAAPTAQSD 180  
 Qy 148 CPPGTAEELKDEVGKGNNHCUPCKAGHFONTSSPARCQPHTRCENQGLVEAAPTAQSD 207  
 ;

QY 181 TTCKNPLELPPPEMSGT 197  
 ;|||||  
 Db 208 TTCKNPLELPPPEMSGT 224

RESULT 8  
 ; Sequence 133, Application US/10262445  
 ; Publication No. US20040104058A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alisobrook II, John  
 ; APPLICANT: Burgess, Catherine  
 ; APPLICANT: Carterton, Elina  
 ; APPLICANT: Chant, John  
 ; APPLICANT: Chaudhuri, Amitabha  
 ; APPLICANT: Gerlach, Valerie  
 ; APPLICANT: Giot, Loic  
 ; APPLICANT: Gorman, Linda  
 ; APPLICANT: Guo, Xiaoja  
 ; APPLICANT: Kekuda, Ramesh  
 ; APPLICANT: Mezes, Peter  
 ; APPLICANT: Millet, Isabelle  
 ; APPLICANT: Ooi, Chean Eng  
 ; APPLICANT: Paturrajan, Meera  
 ; APPLICANT: Riiger, Daniel  
 ; APPLICANT: Spyrek, Kimberly  
 ; APPLICANT: Taupier Jr., Raymond J.  
 ; APPLICANT: Zerhusen, Bryan  
 ; APPLICANT: Zhong, Haibing  
 ; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF USE  
 ; TITLE OF INVENTION: THE SAME  
 ; CURRENT APPLICATION NUMBER: US/10/262,445  
 ; FILE REFERENCE: 21402-462D  
 ; CURRENT FILING DATE: 2002-10-01;  
 ; CURRENT APPLICATION NUMBER: 60/327,454  
 ; PRIOR FILING DATE: 2001-10-05  
 ; PRIOR APPLICATION NUMBER: 60/327,917  
 ; PRIOR FILING DATE: 2001-10-09  
 ; PRIOR APPLICATION NUMBER: 60/328,029  
 ; PRIOR FILING DATE: 2001-10-09  
 ; PRIOR APPLICATION NUMBER: 60/328,056  
 ; PRIOR FILING DATE: 2001-10-09  
 ; PRIOR APPLICATION NUMBER: 60/328,849  
 ; PRIOR FILING DATE: 2001-10-12  
 ; PRIOR APPLICATION NUMBER: 60/329,414  
 ; PRIOR FILING DATE: 2001-10-15  
 ; PRIOR APPLICATION NUMBER: 60/330,142  
 ; PRIOR FILING DATE: 2001-10-17  
 ; PRIOR APPLICATION NUMBER: 60/341,058  
 ; PRIOR FILING DATE: 2001-10-22  
 ; PRIOR APPLICATION NUMBER: 60/343,629  
 ; PRIOR FILING DATE: 2001-10-24  
 ; PRIOR APPLICATION NUMBER: 60/349,575  
 ; PRIOR FILING DATE: 2001-10-29  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 133  
 ; SOFTWARE: Curaséquist version 0.1  
 ; SEQ ID NO: 133  
 ; LENGTH: 435  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-262-445-133

Query Match 99.6%; Score 1129; DB 9; Length 339;  
 Best Local Similarity 99.5%; Pred. No. 3.5e-88; Indels 0; Gaps 0;  
 Matches 196; Conservative 1; Mismatches 0;

QY 1 SQPQAVPPVYASENQCRDQEKEYYEPRHICSRCPGTVYSAKCSRUDTCATAENS 60  
 Db 28 SQPQAVPPVYASENQCRDQEKEYYEPRHICSRCPGTVYSAKCSRUDTCATAENS 87

QY 61 YNEHHWYLITCQLCPDPYMGLEETAPTSKRKUQCRCRCPGMFCAAWALECTCELLSD 120  
 Db 88 YNEHHWYLITCQLCPDPYMGLEETAPTSKRKUQCRCRCPGMFCAAWALECTCELLSD 147

QY 121 CPPGTAEALKDEVGKGNHCVPCKAGHFQNTSSPSARACQPHTRCENQGLVEAAPGTAQSD 180  
 Db 148 CPPGTAEALKDEVGKGNHCVPCKAGHFQNTSSPSARACQPHTRCENQGLVEAAPGTAQSD 207

QY 181 TTCKNPLELPPPEMSGT 197  
 Db 208 TTCKNPLELPPPEMSGT 224

RESULT 9  
 US 09-907-372-1  
 ; Sequence 1, Application US/0907372  
 ; Patent No. US20020061242A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lal, Preeti G.  
 ; TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT  
 ; FILE REFERENCE: PCT-0050 US  
 ; CURRENT APPLICATION NUMBER: US/09/907,372  
 ; CURRENT FILING DATE: 2001-07-27  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 1  
 ; LENGTH: 399  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Incyte ID No. US20020068242A1 7497867CD1  
 ; US-09-907-372-1

Query Match 99.6%; Score 1129; DB 9; Length 339;  
 Best Local Similarity 99.5%; Pred. No. 3.5e-88; Indels 0; Gaps 0;  
 Matches 196; Conservative 1; Mismatches 0;

QY 1 SQPQAVPPVYASENQCRDQEKEYYEPRHICSRCPGTVYSAKCSRUDTCATAENS 60  
 Db 28 SQPQAVPPVYASENQCRDQEKEYYEPRHICSRCPGTVYSAKCSRUDTCATAENS 87

QY 61 YNEHHWYLITCQLCPDPYMGLEETAPTSKRKUQCRCRCPGMFCAAWALECTCELLSD 120  
 Db 88 YNEHHWYLITCQLCPDPYMGLEETAPTSKRKUQCRCRCPGMFCAAWALECTCELLSD 147

QY 121 CPPGTAEALKDEVGKGNHCVPCKAGHFQNTSSPSARACQPHTRCENQGLVEAAPGTAQSD 180  
 Db 148 CPPGTAEALKDEVGKGNHCVPCKAGHFQNTSSPSARACQPHTRCENQGLVEAAPGTAQSD 207

QY 181 TTCKNPLELPPPEMSGT 197  
 Db 208 TTCKNPLELPPPEMSGT 224

RESULT 10  
 US-09-911-372-1  
 ; Sequence 1, Application US/09917372  
 ; Publication No. US200301068619A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lal, Preeti G.  
 ; APPLICANT: Warren, Bridget A.  
 ; TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT  
 ; FILE REFERENCE: PCT-0050 US  
 ; CURRENT APPLICATION NUMBER: US/09/917,372  
 ; CURRENT FILING DATE: 2002-09-09  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 1  
 ; LENGTH: 399  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens

Query Match 100.0%; Score 1133; DB 15; Length 435;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-88; Indels 0; Gaps 0;  
 Matches 197; Conservative 0; Mismatches 0;

QY 1 SPOQAVPPVYASENQCRDQEKEYYEPRHICSRCPGTVYSAKCSRUDTCATAENS 60  
 Db 28 SPOQAVPPVYASENQCRDQEKEYYEPRHICSRCPGTVYSAKCSRUDTCATAENS 87

FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: Incyte ID No. US20030068619A1 7497867CDI.  
US-09-917-372-1

Query Match Best Local Similarity 99.6%; Score 1129; DB 10; Length 399;  
Matches 196; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQPQAVPPYASENQTCRDOKEKEYEYEPQRICCSRCRCPGTYSAKCSRIRDTVCATCAENSNEHWNTITICO 74  
Db 28 SQPQAVPPYASENQTCRDOKEKEYEYEPQRICCSRCRCPGTYSAKCSRIRDTVCATCAENSNEHWNTITICO 87

QY 61 YNEHKNYLTIQOLCRPCDPMGLEBIAPTSKRKTQCRQPGMFCAAWALECTHCELLSD 120  
Db 88 YNEHKNYLTIQOLCRPCDPMGLEBIAPTSKRKTQCRQPGMFCAAWALECTHCELLSD 147

QY 121 CPPGTEAEELKDEVGKGNNCVCPKAGHFRONTSSPSARCOCPHTRCENQGLIVEAARGTAQSD 180  
Db 149 CPPGTEAEELKDEVGKGNNCVCPKAGHFRONTSSPSARCOCPHTRCENQGLIVEAARGTAQSD 207

QY 181 TTCKNPLEPLPPEMSGT 197  
Db 208 TTCKNPLEPLPPEMSGS 224

---

RESULT 11  
US-10-112-793-14  
Sequence 14, Application US/10112793  
Publication No. US20020192729A1

GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94180

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/112-793  
FILING DATE: 28-Mar-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/828,683A  
FILING DATE: 31-Mar-1997  
APPLICATION NUMBER: 08/625328  
FILING DATE: 1-Apr-1996  
APPLICATION NUMBER: 08/710802  
FILING DATE: 23-Sep-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600

REFERENCE DOCKET NUMBER: P1007P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416

INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 170 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-10-112-793-14

Query Match 87.1%; Score 987; DB 13; Length 170;

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RESULT 12  
US-10-315-680-57  
Sequence 57, Application US/10375680  
Publication No. US200400914A1

GENERAL INFORMATION:  
APPLICANT: Ebner, Reinhard  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Ruben, Steven M  
APPLICANT: Ulrich, Stephen  
APPLICANT: Zhai, Yifan

ORGANISM: Homo sapiens

FEATURE:  
NAME/KEY: misc\_feature

LOCATION: (7) -(7)

OTHER INFORMATION: Xaa can be any naturally occurring amino acid

US-10-375-680-57

Query Match Best Local Similarity 85.6%; Score 970; DB 15; Length 172;  
Matches 169; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 15 TCRDOE-KEYKEYEYEPQRICCSRCRCPGTYSAKCSRIRDTVCATCAENSNEHWNTITICO 72  
Db 1 TCRDOEAAEAYEYEPQRICCSRCRCPGTYSAKCSRIRDTVCATCAENSNEHWNTITICO 60

QY 73 LCRPDPVMGLEBIAPTSKRKTQCRQPGMFCAAWALECTHCELLSD 132  
Db 61 LCRPDPVMGLEBIAPTSKRKTQCRQPGMFCAAWALECTHCELLSD 120

QY 133 VKGKNNHCVCPKAGHFRONTSSPSARCOCPHTRCENQGLIVEAARGTAQSDTICK 184  
Db 121 VKGKNNHCVCPKAGHFRONTSSPSARCOCPHTRCENQGLIVEAARGTAQSDTICK 172

---

RESULT 13  
US-09-948-018-19  
Sequence 19, Application US/09948018  
Patent No. US2003015097A1

GENERAL INFORMATION:  
APPLICANT: Theill et al  
TITLE OF INVENTION: TNF RECEPTOR-LIKE MOLECULES AND USES THEREOF  
FILE REFERENCE: 01017/37677  
CURRENT APPLICATION NUMBER: US/09/948,018  
CURRENT FILING DATE: 2001-09-05  
PRIOR APPLICATION NUMBER: US 60/230,191  
PRIOR FILING DATE: 2000-09-05

NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 257  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-948-018-19

Query Match 68.8%; Score 780; DB 9; Length 257;  
Best Local Similarity 100.0%; Pred. No. 1.3e-58; Mismatches 0; Indels 0; Gaps 0;  
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 EHWNLYTICOLCRCPDPVPGLEETAPCTSRRKTCRCCRCGGMFCAAWALECTHRLSDCP 122  
1 EHWNLYTICOLCRCPDPVNGLEETAPCTSRRKTCRCCRCGGMFCAAWALECTHRLSDCP 60

QY 123 PGTRAEKLKRGKGNNHCVPCKAGHONTSSPSARCQPHTRCENQGLVEAAGTAQSDT 182

QY 61 PGTRAEKLKRGKGNNHCVPCKAGHONTSSPSARCQPHTRCENQGLVEAAGTAQSDT 120

Db 183 CKNLPLEPPLPEMSGT 197

Db 121 CKNLPLEPPLPEMSGT 135

RESULT 14

US-10-087-192-939

; Sequence 939, Application US/10087192

; Publication No. US20020182586A1

; GENERAL INFORMATION:

; APPLICANT: Morris, David W.

; APPLICANT: Engelhard, Eric K.

; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR

; FILE REFERENCE: 529452000122

; CURRENT APPLICATION NUMBER: US/10/087, 192

; CURRENT FILING DATE: 2002-03-01

; PRIOR APPLICATION NUMBER: US 09/747, 377

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: US 09/798, 586

; PRIOR FILING DATE: 2001-03-02

; NUMBER OF SEQ ID NOS: 2059

; SOFTWARE: FastSEQ for Windows Version 4.0

; SBQ ID NO 939

; LENGTH: 402

; TYPE: PRT

; ORGANISM: Mus musculus

Query Match 68.0%; Score 771; DB 12; Length 402;

Best Local Similarity 70.7%; Pred. No. 1.2e-57; Mismatches 135; Conservative 14; Mismatches 40; Indels 2; Gaps 1;

Matches 135; Conservative 14; Mismatches 40; Indels 2; Gaps 1;

QY 1 SQPQAVPPYASENCOTCRDPKEFYEPQRHICCSRCPGTVWSAKCSRIRDTCATCAENS 60

41 SQPOLVPPIRNQICWDQKEYEPMHDVCCSRCPGGEFAVCSSRSQDTVKKCPHNS 100

QY 61 YNEHWNLTYTICOLCRCPDPVNGLEETAPCTSRRKTCRCCRCGGMFCAAWALECTHRC-BLL 118

101 YNEHWNLTYTICOLCRCPDPVNGLEETAPCTSRRKTCRCCRCGGMFCAAWALECTHRC-BLL 160

Db 119 SDCEPGTEAKLDEVGKGNNHCVPCKAGHONTSSPSARCQPHTRCENQGLVEAAGTAQ 178

161 VLCQPGTEARVTDIEMDITDVNCVPCKPGHQNTSSPRARCQPHTRCENQGLVEAAGTSY 207

QY 179 SDTICKNPLRP 189

Db 208 SDTICKNPLRP 218

Search completed: August 28, 2004, 01:53:06

Job time : 128 secs

Patent No. US20010021516A1  
; GENERAL INFORMATION:  
; APPLICANT: Wei, Ying-Fei  
; APPLICANT: Gentz, Reiner  
; APPLICANT: Ruben, Steven  
; APPLICANT: Ni, Jian  
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5  
; FILE REFERENCE: 1488-1280006  
; CURRENT APPLICATION NUMBER: US/09/826, 212  
; CURRENT FILING DATE: 2001-04-05  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn version 3.0  
; SBQ ID NO 6  
; LENGTH: 415  
; TYPE: RT  
; ORGANISM: Homo sapiens  
US-09-826-212-6

Query Match 68.0%; Score 771; DB 9; Length 415;  
Best Local Similarity 70.7%; Pred. No. 1.2e-57; Mismatches 40; Indels 2; Gaps 1;  
Matches 135; Conservative 14; Mismatches 40; Indels 2; Gaps 1;

QY 1 SQPQAVPPYASENCOTCRDPKEFYEPQRHICCSRCPGTVWSAKCSRIRDTCATCAENS 60

Db 28 SQPOLVPPIRNQICWDQKEYEPMHDVCCSRCPGGEFAVCSSRSQDTVKKCPHNS 87

QY 61 YNEHWNLTYTICOLCRCPDPVNGLEETAPCTSRRKTCRCCRCGGMFCAAWALECTHRC-BLL 118

88 YNEHWNLTYTICOLCRCPDPVNGLEETAPCTSRRKTCRCCRCGGMFCAAWALECTHRC-BLL 147

Db 119 SDCEPGTEAKLDEVGKGNNHCVPCKAGHONTSSPSARCQPHTRCENQGLVEAAGTAQ 178

148 VLCQPGTEARVTDIEMDITDVNCVPCKPGHQNTSSPRARCQPHTRCENQGLVEAAGTSY 207

QY 179 SDTICKNPLRP 189

Db 208 SDTICKNPLRP 218

RESULT 15

US-09-826-212-6

; Sequence 6, Application US/09826212